





1b 61 trlqqulthfrthsrtdqthrrtnqskss 96

#### RESULT 4

AAW99819 standard: protein; 96 AA.

AAW99819:

08-JUN-1999 (first entry)

HIV A549 protein sequence.

HIV Vpr: human immunodeficiency virus: hyperproliferative disease, cell proliferation.

Human immunodeficiency virus

W09909412-A1.

25-FEB-1999.

14-AUG-1998: 98W0-0816890.

14-AUG-1997: 97US-0055764.

(TYPE: ) UNIV HINNSTAVARIA.

AYYGVGVV V. Klobner-Emmense T. Mahalingam S. Patel M.

W099181154/15.

Conjugate composition comprising HIV-1 Vpr protein fragment used

to inhibit cell proliferation, and treating hyperproliferative

diseases

Example: Fig 1B: 64pp; English.

The present invention describes a conjugate composition comprising a treatment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic compound. The conjugate can be used to a method for inhibiting cell proliferation. It can also be used for treating an individual who has a hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein fragments can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents an HIV protein sequence.

Sequence 96 AA:

Query Match 94.8%; Score 499; DB 20; Length 96;

Best Local Similarity 95.8%; Prod. No. 2, 50-53;

Methods 92; Conserved 1; Mismatch 4; Indels 0; Gaps 0;

1 MEQAPEDQPRVPMWTELEEKNEAVRHPKMLHSQHYFYGMWGVAL 60

1 meqpedqprvpmwteleekneavrhpkmhslsqhyfygmwgvall 60

61 trlqqulthfrthsrtdqthrrtnqskss 96

61 trlqqulthfrthsrtdqthrrtnqskss 96

AAW99819 standard: protein; 96 AA.

AAW99819:

08-JUN-1999 (first entry)

HIV A549 protein sequence.

Human immunodeficiency virus

W09909412-A1.

XX HIV: Vpr: human immunodeficiency virus: hyperproliferative disease;

cell proliferation.

Human immunodeficiency virus.

W09909412-A1.

25-FEB-1999.

14-AUG-1998: 98W0-0816890.

14-AUG-1997: 97US-0055764.

(TYPE: ) UNIV HINNSTAVARIA.

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W099181154/15.

Conjugate composition comprising HIV-1 Vpr protein fragment used

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Example: Fig 1B: 64pp; English.

The present invention describes a conjugate composition comprising a treatment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic compound. The conjugate can be used in a method for inhibiting cell proliferation. It can also be used for treating an individual who has a hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein fragments can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents an HIV protein sequence.

Sequence 96 AA:

Query Match 94.8%; Score 488; DB 20; Length 96;

Best Local Similarity 95.8%; Prod. No. 4, 40-53;

Methods 92; Conserved 2; Mismatch 4; Indels 0; Gaps 0;

1 MEQAPEDQPRVPMWTELEEKNEAVRHPKMLHSQHYFYGMWGVAL 60

1 meqpedqprvpmwteleekneavrhpkmhslsqhyfygmwgvall 60

61 trlqqulthfrthsrtdqthrrtnqskss 96

61 trlqqulthfrthsrtdqthrrtnqskss 96

AAW99820 standard: protein; 96 AA.

AAW99820:

08-JUN-1999 (first entry)

HIV A549 protein sequence.

HIV: Vpr: human immunodeficiency virus: hyperproliferative disease;

cell proliferation.

Human immunodeficiency virus.

W09909412-A1.

25-FEB-1999.

14-AUG-1998: 98W0-0816890.













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GM protein - protein search, using sw model

Run on: October 3, 2001, 13:20:57 : Search time 91.69 seconds

(without alignment)  
51,474 Million of database

Hit:  
Perfect score: 518  
Sequence: 1 MegaProteinDatabase.....US0805421-1:US0805421-1:96

Scoring table:  
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Gap: 10 0, Offset: 0.5  
Search: 2503250 seqs, 21847457 residues  
Total number of hits satisfying chosen parameters: 2863429

Minimum hit seq length: 0  
Maximum hit seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: Pending\_Patents\_AA-Meio\*

1	US-09-412-863-1:US-09-412-863-1:96	1
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Prod. No. is the number of results produced by software. If Prod. No. is greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	470	96.7	96	18	US-09-454-156-1	Sequence 1, Appl 1
3	470	96.7	96	18	US-09-454-156-1	Sequence 1, Appl 1
4	461	89.0	96	11	US-08-700-408-1	Sequence 1, Appl 1
5	461	89.0	96	11	US-08-700-408-1	Sequence 1, Appl 1
6	461	89.0	96	11	US-08-700-408-1	Sequence 1, Appl 1
7	461	89.0	96	11	US-08-700-408-1	Sequence 1, Appl 1
8	461	89.0	96	11	US-08-700-408-1	Sequence 1, Appl 1
9	461	89.0	96	11	US-08-700-408-1	Sequence 1, Appl 1
10	461	89.0	96	11	US-08-700-408-1	Sequence 1, Appl 1

11	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
12	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
13	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
14	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
15	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
16	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
17	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
18	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
19	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
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24	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
25	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
26	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
27	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
28	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
29	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
30	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
31	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
32	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
33	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1
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45	361	69.7	72	18	US-09-454-156-4	Sequence 4, Appl 1



|||||  
 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96

# RESULT 4

US-09-700-408 67

Sequence 67, Application US/09700409  
 GENERAL INFORMATION:  
 APPLICANT: Acad. Almad A.  
 APPLICANT: Macrodio, Jan G.  
 APPLICANT: Armadillo, Chinch  
 TITLE OF INVENTION: VPS AND VPS PROTEINS OF HIV  
 NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:  
 ADDRESS: 400 SEVENTH STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: U.S.A.

ZIP: 20004  
 COUNTRY: U.S.A.  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compat 100  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09-730,408  
 FILING DATE: 25-NOV-1996  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: AU 941697  
 FILING DATE: 25-MAR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: AU 941697  
 FILING DATE: 25-MAR-1994

ATTORNEY, COUNSEL, AND AGENT:  
 NAME: Holman, John G.  
 REGISTRATION NUMBER: 22,769  
 REPRESENTED BY: MEMBER 9944, 198586000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-692-6542  
 TELEFAX: 202-692-6530  
 INFORMATION FOR SEQ ID NO: 67:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 STRANDNESS:  
 TOPLOGY: Linear  
 MOLECULE TYPE: Peptide  
 US-09-700-408-17

Query Match 89.0%, Score 461, DB 11, Length 96  
 Best local similarity 87.5%, Field No 49  
 Matches 84: Conservative 7, Mismatches 5, Indels 0, Gaps 0

QY 1 MEOAEPDGPPEPPYNNWTELELEKNEAVRPPIWLSIOGHVETGDTWVGEAL 60  
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 1 MEOAEPDGPPEPPYNNWTELELEKNEAVRPPIWLSIOGHVETGDTWVGEAL 60  
 DB 1 MEOAEPDGPPEPPYNNWTELELEKNEAVRPPIWLSIOGHVETGDTWVGEAL 60  
 QY 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96  
 |||||  
 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96  
 DB 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96

# RESULT 5

US-09-309-572-19

Sequence 19, Application US/09309572  
 GENERAL INFORMATION:  
 APPLICANT: Helix-Helix Institute  
 APPLICANT: Helix-Helix Institute  
 TITLE OF INVENTION: A Recombinant Hybrid Vaccine Pseudotyped with HCMV  
 FILE REFERENCE: P50489  
 CURRENT APPLICATION NUMBER: US/09-406 572

|||||  
 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96

# RESULT 6

US-09-718-096-19

Sequence 19, Application US/09718096  
 GENERAL INFORMATION:  
 APPLICANT: Von Loer, Melke-Dorthea  
 TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH HCMV  
 FILE REFERENCE: 45-195  
 REGISTRATION NUMBER: 200-11-22  
 REPRESENTED BY: MEMBER 9944, 198586000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-692-6542  
 TELEFAX: 202-692-6530  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 STRANDNESS:  
 TOPLOGY: Linear  
 MOLECULE TYPE: Peptide  
 US-09-718-096-19

Query Match 89.0%, Score 461, DB 21, Length 96  
 Best local similarity 87.5%, Field No 49  
 Matches 84: Conservative 7, Mismatches 5, Indels 0, Gaps 0

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 |||||  
 1 MEOAEPDGPPEPPYNNWTELELEKNEAVRPPIWLSIOGHVETGDTWVGEAL 60  
 DB 1 MEOAEPDGPPEPPYNNWTELELEKNEAVRPPIWLSIOGHVETGDTWVGEAL 60  
 QY 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96  
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 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96  
 DB 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96

# RESULT 7

US-09-422-917A-19

Sequence 19, Application US/09422917A  
 GENERAL INFORMATION:  
 APPLICANT: Delaport, Eric  
 APPLICANT: Delaport, Eric  
 TITLE OF INVENTION: A Recombinant Hybrid Vaccine Pseudotyped with HCMV  
 FILE REFERENCE: P50489  
 CURRENT APPLICATION NUMBER: US/09-406 572

Query Match 89.0%, Score 461, DB 21, Length 96  
 Best local similarity 87.5%, Field No 49  
 Matches 84: Conservative 7, Mismatches 5, Indels 0, Gaps 0

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 1 MEOAEPDGPPEPPYNNWTELELEKNEAVRPPIWLSIOGHVETGDTWVGEAL 60  
 DB 1 MEOAEPDGPPEPPYNNWTELELEKNEAVRPPIWLSIOGHVETGDTWVGEAL 60  
 QY 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96  
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 DB 61 IRIIGQILFIRIPICGPHSPICVTPPPAANVCASS 96

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 15-0224 **3,4,5-ATTA-142**  
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 15-0227 **3,4,5-ATTA-145**  
 15-0228 **3,4,5-ATTA-146**  
 15-0229 **3,4,5-ATTA-147**  
 15-0230 **3,4,5-ATTA-148**  
 15-0231 **3,4,5-ATTA-149**  
 15-0232

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Search completed: 10/10/2014 14:21:27  
Job time: 160 sec





1 CURRENT FILING DATE: 1998-07-30  
 2 PRIOR APPLICATION NUMBERS: PCT/JP95/00191  
 3 PRIOR FILING DATE: 1995-04-19  
 4 INVENTOR: COHEN, ERIC A.  
 5 INVENTOR: BERGERON, DOMINIQUE  
 6 INVENTOR: YAO, XIAO-JIAN  
 7 SFWARE: Patentia version 3.0  
 8 SEQ ID NO: 5  
 9 LENGTH: 78  
 10 TYPE: PRT  
 11 ORGANISM: Human immunodeficiency virus type 1  
 12 US-09-421-900-5

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 2 1 MEQAFEDGPGFPPRNTETLLEKNAVRPRPRWISQHYVYGVQWVAVAI 60  
 3 61 IRILOOLLPIHF 73  
 4 61 IRILOOLLPIHF 73

RESULT 5  
 US-08-401-915-4

1 Sequence 4, Application US/08401915  
 2 Patent No. 5811101  
 3 GENERAL INFORMATION:  
 4 APPLICANT: COHEN, ERIC A.  
 5 APPLICANT: BERGERON, DOMINIQUE  
 6 APPLICANT: CHECKERONE, FLORENT  
 7 APPLICANT: YAO, XIAO-JIAN  
 8 ADDRESS: 10000 KENNEDY, GARY  
 9 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS  
 10 TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES  
 11 NUMBER OF SEQUENCES: 5  
 12 CORRESPONDENCE ADDRESSES:  
 13 ADDRESSEE: KLAUDER & JACKSON  
 14 STREET: 6061000001 Plaza, 111 Hickensack Avenue  
 15 CITY: Hackensack  
 16 STATE: N.J.  
 17 COUNTRY: U.S.A.  
 18 ZIP: 07601  
 19 TELEPHONE: 201-487-5800  
 20 TELEFAX: 201-443-1664  
 21 FAX: 134921  
 22 INFORMATION FOR SEQ ID NO: 4:  
 23 SEQUENCE CHARACTERISTICS:  
 24 LENGTH: 72 amino acids  
 25 TYPE: amino acid  
 26 STRANDEDNESS: single  
 27 TOPOLOGY: linear  
 28 MOLECULE TYPE: protein  
 29 HYPOTHEICAL: NO  
 30 US-08-401-915-4

Query Match: 69.7% Score 461 PB 2: Length 72:

Best Local Similarity: 91.7% Prod. No. 1.9e-49  
 Matches: 66 Mismatches: 2 Indels: 4 Gaps: 0  
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 4 61 IRILOOLLPIHF 72

RESULT 6  
 US-08-524-694A-4

1 Sequence 4, Application: US/08524694A  
 2 Patent No. 6043081  
 3 GENERAL INFORMATION:  
 4 APPLICANT: COHEN, ERIC A.  
 5 APPLICANT: BERGERON, DOMINIQUE  
 6 APPLICANT: CHECKERONE, FLORENT  
 7 APPLICANT: YAO, XIAO-JIAN  
 8 ADDRESS: 10000 KENNEDY, GARY  
 9 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED  
 10 TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES  
 11 NUMBER OF SEQUENCES: 5  
 12 CORRESPONDENCE ADDRESSES:  
 13 ADDRESSEE: KLAUDER & JACKSON  
 14 STREET: 6061000001 Plaza, 111 Hickensack Avenue  
 15 CITY: Hackensack  
 16 STATE: N.J.  
 17 COUNTRY: U.S.A.  
 18 ZIP: 07601  
 19 TELEPHONE: 201-487-5800  
 20 TELEFAX: 201-443-1664  
 21 FAX: 134921  
 22 INFORMATION FOR SEQ ID NO: 4:  
 23 SEQUENCE CHARACTERISTICS:  
 24 LENGTH: 72 amino acids  
 25 TYPE: amino acid  
 26 STRANDEDNESS: single  
 27 TOPOLOGY: linear  
 28 MOLECULE TYPE: protein  
 29 HYPOTHEICAL: NO  
 30 US-08-524-694A-4

Query Match: 69.7% Score 461 PB 3: Length 72:

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 3 61 IRILOOLLPIHF 72  
 4 61 IRILOOLLPIHF 72

RESULT 7



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RESULT 10
US-09-485-421-1
Sequence 9, Application US/094649251
Patent No. 5863081
GENERAL INFORMATION:
APPLICANT: Kraus, Guenther
APPLICANT: Wang-Staal, Flossie
APPLICANT: Talbot, Randy
APPLICANT: Foeschla, Eric
TITLE OF INVENTION: Isolation of No. 5863081 HIV 2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/MS-DOS
SOFTWARE: Patented Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/094649251
FILING DATE: No. 5863081 yet assigned
CLASSIFICATION: C11
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,441
FILING DATE: 26-JUL-1995
ALORNEY/AGENT INFORMATION:
NAME: Carrell-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS:
ISOPHASE: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1..105
OTHER INFORMATION: /note- "Ypr protein encoded by HIV 2KR"
US-09-485-421-1
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DB 66 INVADALVIRKACKSKRIG 87
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RESULT 12
US-09-485-421-1
Sequence 9, Application US/094649251
Patent No. 5863081
GENERAL INFORMATION:
APPLICANT: Kraus, Guenther
APPLICANT: Wang-Staal, Flossie
APPLICANT: Talbot, Randy
APPLICANT: Foeschla, Eric
TITLE OF INVENTION: Isolation of No. 5863081 HIV 2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/MS-DOS
SOFTWARE: Patented Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,490
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/094649251
FILING DATE:
ALORNEY/AGENT INFORMATION:
NAME: Carrell-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS:
ISOPHASE: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1..105
OTHER INFORMATION: /note- "Ypr protein encoded by HIV 2KR"
US-09-256-490-9
Query Match 36.1% Score 187; DB 4; Length 105;
Best Local Similarity 46.3% Freq. No. 8.1e-17;
Matches 38; Conservative 16; Mismatches 22; Indels 2; Gaps 2;
QY 2 EQAPETQCPPEYPMWTLLEELKNEAVRH-PRMLSHDAHLYTYGDTWVEAL 60
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1 NAME: BELUCA, MARK
2 REGISTRATION NUMBER: 34, 279
3 KEYWORD: 27-28-29-30-31-32-33-34-35-36-37-38-39-40-41-42-43-44-45-46-47-48-49-50-51-52-53-54-55-56-57-58-59-60-61-62-63-64-65-66-67-68-69-70-71-72-73-74-75-76-77-78-79-80-81-82-83-84-85-86-87-88-89-90-91-92-93-94-95-96-97-98-99-100-101-102-103-104-105-106-107-108-109-110-111-112-113-114-115-116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000-1001-1002-1003-1004-1005-1006-1007-1008-1009-1010-1011-1012-1013-1014-1015-1016-1017-1018-1019-1020-1021-1022-1023-1024-1025-1026-1027-1028-1029-1030-1031-1032-1033-1034-1035-1036-1037-1038-1039-1040-1041-1042-1043-1044-1045-1046-1047-1048-10
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RESULT 14  
 OCT-0593-04301-1  
 Submitted by: Applicant 006 PG/T059304301  
 GENERAL INFORMATION:  
 1 APPLICANT: MYTON E. ESSOX et al.  
 2 TITLE OF INVENTION: AIDS Therapeutics Based on HIV-2  
 3 TITLE OF INVENTION: HIV Therapies  
 4 NUMBER OF SEQUENCES: 8  
 5 CORRESPONDENT ADDRESS:  
 6 ADDRESSEE: Fish & Richardson  
 7 STREET: 225 Franklin Street  
 8 CITY: Boston  
 9 STATE: MA  
 10 COUNTRY: U.S.A.  
 11 ZIP: 02110-2804  
 12 COMPUTER READABLE FORM:  
 13 MEDIUM TYPE: floppy disk  
 14 OPERATING SYSTEM: PC-DOS/MS-DOS  
 15 SOFTWARE: Patent in Release #1.0, Version #1.25  
 16 CURRENT APPLICATION DATA:  
 17 APPLICATION NUMBER: PCT/US93/04301  
 18 FILING DATE: 19930507  
 19 CLASSIFICATION:  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Peromato, John W.  
 22 REGISTRATION NUMBER: 29,066  
 23 RESIDENT CITY STATE ZIP: 173, 07301  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: 617/542-5070  
 26 TELEFAX: 617/542-8906  
 27 INFORMATION FOR SEQUENCE 1:  
 28 SEQUENCE CHARACTERISTICS:  
 29 LENGTH: 112  
 30 TYPE: ANTI-CD4  
 31 STANDARDS:  
 32 TOTAL SIZE: 110001  
 33 PCT-0593-04301-1

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									GapS
Q7	17	QWLLLELLHKNVAPHTPRIMLSLSQHYIYNDIWTQENALR	----	11QQLLELLH	71				
	211	211	111	11	1	1	1	1	1
136	25	EMINLEINLENNENAVNIIPLGLI	12AVVLP	456	500	2	395	25	13
	25	25	111	11	1	1	1	1	1
77	72	ELIQR	77						





1

2

3

GenCore version 4.5  
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com protein - protein search, using sw model

Received: October 3, 2001; 13:20:57. Accepted: June 14, 2002.

(wilcox et al.) experiment 1

489.148 Million cell updates/sec

Title: US-09-485-421-1

Perfect score: 518  
Score: 1 MEQA PEDDOGORY UNIT

Sequence: 1 MEQAVPEIQGSPURPYPIWT

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Severing + 4k10

Gap: 10.0 , GapExt: 0.5

014341 5000 76174557

searched:	219241 seqs, 76174552 residues
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Parameter	Value
Total number of hits satisfying chosen parameters:	21/24

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Minimum DB seq length: 0
Maximum Efs seq length: 2000000000
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Post-processing: Minimum Match, 0%

Maximum Match: 100%

Listed first 45 Summary first

Juliano

Dir:

01112: \*

Environ Monit Assess (2008) 142:111–120

## SUMMARY

pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Correct Match	Length	DB	ID	Accession
1	459	68.6	96	2	104434	VP1 protein - human
2	454	67.6	96	2	56480	VP1 protein - human
3	448.6	67.6	97	1	24333	VP1 protein - human
4	445	85.9	96	2	T01670	VP1 protein - human
5	441.5	85.2	95	2	15323	VP1 protein - human
6	402	77.6	96	1	ASL18C	VP1 protein - sim
7	248	47.9	97	2	S03057	accessory protein - sim
8	248	47.9	101	1	ASL18B	VP1 protein - sim
9	247	47.7	89	2	S07991	VP1 protein - sim
10	245.5	47.4	101	2	T1154	VP1 protein - sim
11	243.5	47.0	122	1	ASL18S	VP1 protein - sim
12	235	45.5	165	2	650056	VP1 protein - human
13	224	44.2	101	2	S08439	VP1 protein - human
14	221.5	42.8	104	1	ASL1J	VP1 protein - human
15	214.5	41.4	105	1	ASL1J2	VP1 protein - human
16	210	40.5	104	1	ASL1J	VP1 protein - human
17	207	40.2	165	2	S21256	VP1 protein - human
18	204	39.4	105	1	ASL18B	VP1 protein - human
19	193	39.5	104	2	S28081	VP1 protein - human
20	97.5	19.1	140	2	S28081	VP1 protein - sim
21	97.5	18.8	119	1	ASL18J	VP1 protein - sim
22	93.5	18.1	112	1	ASL18J	VP1 protein - sim
23	92.6	17.6	112	2	S20966	VP1 protein - sim
24	90.5	17.5	112	2	ASL1J	VP1 protein - sim
25	84.5	16.3	112	1	ASL18B	VP1 protein - sim
26	81.5	16.3	112	2	S07991	VP1 protein - sim
27	81.5	16.1	112	2	S1154	VP1 protein - sim
28	81	16.0	112	2	T1154	VP1 protein - sim
29	76.8	15.9	112	1	ASL1J	VP1 protein - sim

[illegible]

[illegible][illegible][illegible]

Received 4 July 2000  
 Accepted 1 February 2001

**Key words:** human immunodeficiency virus type 1, phylogenetic, human immunodeficiency virus type 1, antibody, 1980s, reproductive coercion, risk, HIV-1, cross-sectional study.

**Abbreviations:** HIV-1, human immunodeficiency virus type 1; 1980s, 1980–1989; 1990s, 1990–1999; 2000s, 2000–2009; 2010s, 2010–2019; 2020s, 2020–2029; 2030s, 2030–2039; 2040s, 2040–2049; 2050s, 2050–2059; 2060s, 2060–2069; 2070s, 2070–2079; 2080s, 2080–2089; 2090s, 2090–2099; 2100s, 2100–2109; 2110s, 2110–2119; 2120s, 2120–2129; 2130s, 2130–2139; 2140s, 2140–2149; 2150s, 2150–2159; 2160s, 2160–2169; 2170s, 2170–2179; 2180s, 2180–2189; 2190s, 2190–2199; 2200s, 2200–2209; 2210s, 2210–2219; 2220s, 2220–2229; 2230s, 2230–2239; 2240s, 2240–2249; 2250s, 2250–2259; 2260s, 2260–2269; 2270s, 2270–2279; 2280s, 2280–2289; 2290s, 2290–2299; 2300s, 2300–2309; 2310s, 2310–2319; 2320s, 2320–2329; 2330s, 2330–2339; 2340s, 2340–2349; 2350s, 2350–2359; 2360s, 2360–2369; 2370s, 2370–2379; 2380s, 2380–2389; 2390s, 2390–2399; 2400s, 2400–2409; 2410s, 2410–2419; 2420s, 2420–2429; 2430s, 2430–2439; 2440s, 2440–2449; 2450s, 2450–2459; 2460s, 2460–2469; 2470s, 2470–2479; 2480s, 2480–2489; 2490s, 2490–2499; 2500s, 2500–2509; 2510s, 2510–2519; 2520s, 2520–2529; 2530s, 2530–2539; 2540s, 2540–2549; 2550s, 2550–2559; 2560s, 2560–2569; 2570s, 2570–2579; 2580s, 2580–2589; 2590s, 2590–2599; 2600s, 2600–2609; 2610s, 2610–2619; 2620s, 2620–2629; 2630s, 2630–2639; 2640s, 2640–2649; 2650s, 2650–2659; 2660s, 2660–2669; 2670s, 2670–2679; 2680s, 2680–2689; 2690s, 2690–2699; 2700s, 2700–2709; 2710s, 2710–2719; 2720s, 2720–2729; 2730s, 2730–2739; 2740s, 2740–2749; 2750s, 2750–2759; 2760s, 2760–2769; 2770s, 2770–2779; 2780s, 2780–2789; 2790s, 2790–2799; 2800s, 2800–2809; 2810s, 2810–2819; 2820s, 2820–2829; 2830s, 2830–2839; 2840s, 2840–2849; 2850s, 2850–2859; 2860s, 2860–2869; 2870s, 2870–2879; 2880s, 2880–2889; 2890s, 2890–2899; 2900s, 2900–2909; 2910s, 2910–2919; 2920s, 2920–2929; 2930s, 2930–2939; 2940s, 2940–2949; 2950s, 2950–2959; 2960s, 2960–2969; 2970s, 2970–2979; 2980s, 2980–2989; 2990s, 2990–2999; 3000s, 3000–3009; 3010s, 3010–3019; 3020s, 3020–3029; 3030s, 3030–3039; 3040s, 3040–3049; 3050s, 3050–3059; 3060s, 3060–3069; 3070s, 3070–3079; 3080s, 3080–3089; 3090s, 3090–3099; 3100s, 3100–3109; 3110s, 3110–3119; 3120s, 3120–3129; 3130s, 3130–3139; 3140s, 3140–3149; 3150s, 3150–3159; 3160s, 3160–3169; 3170s, 3170–3179; 3180s, 3180–3189; 3190s, 3190–3199; 3200s, 3200–3209; 3210s, 3210–3219; 3220s, 3220–3229; 3230s, 3230–3239; 3240s, 3240–3249; 3250s, 3250–3259; 3260s, 3260–3269; 3270s, 3270–3279; 3280s, 3280–3289; 3290s, 3290–3299; 3300s, 3300–3309; 3310s, 3310–3319; 3320s, 3320–3329; 3330s, 3330–3339; 3340s, 3340–3349; 3350s, 3350–3359; 3360s, 3360–3369; 3370s, 3370–3379; 3380s, 3380–3389; 3390s, 3390–3399; 3400s, 3400–3409; 3410s, 3410–3419; 3420s, 3420–3429; 3430s, 3430–3439; 3440s, 3440–3449; 3450s, 3450–3459; 3460s, 3460–3469; 3470s, 3470–3479; 3480s, 3480–3489; 3490s, 3490–3499; 3500s, 3500–3509; 3510s, 3510–3519; 3520s, 3520–3529; 3530s, 3530–3539; 3540s, 3540–3549; 3550s, 3550–3559; 3560s, 3560–3569; 3570s, 3570–3579; 3580s, 3580–3589; 3590s, 3590–3599; 3600s, 3600–3609; 3610s, 3610–3619; 3620s, 3620–3629; 3630s, 3630–3639; 3640s, 3640–3649; 3650s, 3650–3659; 3660s, 3660–3669; 3670s, 3670–3679; 3680s, 3680–3689; 3690s, 3690–3699; 3700s, 3700–3709; 3710s, 3710–3719; 3720s, 3720–3729; 3730s, 3730–3739; 3740s, 3740–3749; 3750s, 3750–3759; 3760s, 3760–3769; 3770s, 3770–3779; 3780s, 3780–3789; 3790s, 3790–3799; 3800s, 3800–3809; 3810s, 3810–3819; 3820s, 3820–3829; 3830s, 3830–3839; 3840s, 3840–3849; 3850s, 3850–3859; 3860s, 3860–3869; 3870s, 3870–3879; 3880s, 3880–3889; 3890s, 3890–3899; 3900s, 3900–3909; 3910s, 3910–3919; 3920s, 3920–3929; 3930s, 3930–3939; 3940s, 3940–3949; 3950s, 3950–3959; 3960s, 3960–3969; 3970s, 3970–3979; 3980s, 3980–3989; 3990s, 3990–3999; 4000s, 4000–4009; 4010s, 4010–4019; 4020s, 4020–4029; 4030s, 4030–4039; 4040s, 4040–4049; 4050s, 4050–4059; 4060s, 4060–4069; 4070s, 4070–4079; 4080s, 4080–4089; 4090s, 4090–4099; 4100s, 4100–4109; 4110s, 4110–4119; 4120s, 4120–4129; 4130s, 4130–4139; 4140s, 4140–4149; 4150s, 4150–4159; 4160s, 4160–4169; 4170s, 4170–4179; 4180s, 4180–4189; 4190s, 419

ID# 611875061LE1H9P3GHSK111BOKRANOSSES 96

RESULT 5

109484

gpt protein - human immunodeficiency virus type 1 (isolate cut1.1)

c-Spectrum: human immunodeficiency virus type 1, HIV-1

A.Variety: isolate cut1.1

C.Growth: 11-Jun-1999, aspermyr, resolution: 11-Jun-1999 #1-XL;Changco ZJ-Jul-2000

V.Accession: 109484

R.Mitchell, N.L.; Chan, G.; d'Arcy, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.

1. Virus: 69% 4228 428%, 1995

A.II: 11-1995; accession: 109484; Name: A human immunodeficiency virus type 1 infected

A.Reference number: Z16654; MIDB:95287475

A.Accession: 109484

A.Status: preliminary; translated from cbyEMBL/DBPI

A.Molecule type: tNA

A.Restricted: 1.95 %M<sup>2</sup>

A.Coverage: 100%;Genome: EMBL:U24451; MIDB:954440; PINN:AAA9575; 1; FID:GB20444

C.Gene loc:

A.Name: vif

A.Superfamily: AIDS vpr protein

C.Keywords: AIDS; immunodeficiency

[illegible]

**RESULTS**  
**AST-SD**  
 vpr protein - simian immunodeficiency virus SIVcpz  
 N.A. protein names: vif-R protein  
 5. Species: simian immunodeficiency virus SIVcpz  
 A. Name: host Pan troglodytes (chimpanzee)  
 6. Date: 30 Sep 1991 #sequence revision to Sep-1991  
 7. Accession: S09946  
 8. Ref: 1.2. Clayton, R.; Meyerhans, A.; Roizants, U.; Wain-Hobson, S.  
 Nature 345, 456-459, 1990  
 A. Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
 A. Accession number: S09946; M01D0029937  
 A. Accession: S09946  
 A. Status: nucleotide sequence not shown; translation not shown  
 A. Molecule type: RNA  
 A. Restriction: 1-96 + HNA  
 A. Cross references: EMBL:X52154; NID:058866; FID:04A0404.1; PID:058870  
 9. Genbank: 1  
 A. Name: vpr  
 5. Superfamily: AIDS vpr protein  
 7. Keywords: AIDS; immunodeficiency

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Post Local Stationary	81.161	Prod. No. H-76-422		
Michigan	922	1st quarter 1970	62	Index 8
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1	MEAGAN, E. J.	YOUNG, J. L.	KNIGHT, J. L.	THE HISTORY OF THE STATE OF
2	ALABAMA	1811	1811	1811
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[illegible]













[illegible]







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151
152 SOURCE: FROM N.A.
153 STRAIN ISOLATE PV22;
154 MEDID: 8511157; Pubmed 2982104;
155 Muehlen M.A., Smith D.H., Cabralilla C.D., Benton C.V., Lasky L.A.,
156 Capon D.J.
157 "Nucleic acid structure and expression of the human
158 AIDS-2 lymphadenopathy retrovirus."
159 Nature 343:450-456(1985).
160
161 This SWISS-Prot entry is copyrighted. It is produced through a collaboration
162 between the Swiss Institute of Bioinformatics and the EMBL institution.
163 The European Bioinformatics Institute, there are no restrictions on its
164 use by non profit institutions as long as its content is in no way
165 modified and this statement is not removed, changed by and for commercial
166 purposes or linked to a commercial account (see http://www.ssi.unibe.ch/
167 or send an email to ilconso@isb.ssi.ch).
168
169 EMBL: K02083; AAB56669.1;
170 EMBL: M15654; AAA44264.1;
171 EMBL: X01762; NOT_ANNOTATED_CDS.
172 EMBL: K01455; AAB50261.1;
173 EMBL: M11640; AAA44998.1;
174 EMBL: M14100; AAA44675.1;
175 HIV: M15654; VPSHB102.
176 HIV: M14100; VPSHBX4.
177 HIV: K02083; VPSHV22.
178 HIV: K04455; VPSHBX2.
179 HIV: M11640; VPSHBV12.
180
181 Genbank: F000522; VPR: 1.
182 PRINSE: F00444; HIVVPRVX.
183 AIDS.
184 SOURCE: 78 AA; 9405 MB; 145600073AATP64 CDS(4);
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152 SOURCE: FROM N.A.
153 STRAIN ISOLATE PV22;
154 MEDID: 8511157; Pubmed 2982104;
155 Muehlen M.A., Smith D.H., Cabralilla C.D., Benton C.V., Lasky L.A.,
156 Capon D.J.
157 "Nucleic acid structure and expression of the human
158 AIDS-2 lymphadenopathy retrovirus."
159 Nature 343:450-456(1985).
160
161 This SWISS-Prot entry is copyrighted. It is produced through a collaboration
162 between the Swiss Institute of Bioinformatics and the EMBL institution.
163 The European Bioinformatics Institute, there are no restrictions on its
164 use by non profit institutions as long as its content is in no way
165 modified and this statement is not removed, changed by and for commercial
166 purposes or linked to a commercial account (see http://www.ssi.unibe.ch/
167 or send an email to ilconso@isb.ssi.ch).
168
169 EMBL: K02083; AAB56669.1;
170 EMBL: M15654; AAA44264.1;
171 EMBL: X01762; NOT_ANNOTATED_CDS.
172 EMBL: K01455; AAB50261.1;
173 EMBL: M11640; AAA44998.1;
174 EMBL: M14100; AAA44675.1;
175 HIV: M15654; VPSHB102.
176 HIV: M14100; VPSHBX4.
177 HIV: K02083; VPSHV22.
178 HIV: K04455; VPSHBX2.
179 HIV: M11640; VPSHBV12.
180
181 Genbank: F000522; VPR: 1.
182 PRINSE: F00444; HIVVPRVX.
183 AIDS.
184 SOURCE: 78 AA; 9405 MB; 145600073AATP64 CDS(4);
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DB 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

RESULT 15

Q9E246 PRELIMINARY PRT 96 AA

AC Q9E246

DT 01-MAR-2001 (EMBLrel. 16, created)

DE 01-MAR-2001 (EMBLrel. 16, last sequence update)

DE 01-MAR-2001 (EMBLrel. 16, last annotation update)

DE VPR Protein (FRAGMENT).

GN VPR.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID:11676;

LN 111

RF SEQUENCE FROM N.A.

RC STRAIN:M14.4;

RA Ahmad N., Yedavalli V.S.R.K.;

RT "Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical Transmission."

RI Submitted (09F-2000) to the EMBO/GenBank/TrnB database.

RI EMBL: AF275119; AAC32771;

RI NON-TER 96

FT SEQUENCE 96 AA: 11488 MW: 068DF9C875166810 CRC64:

Query Match 90.7% Score 470; DR 14; Length 96;  
 Best Local Similarity 89.6%; Pred. No. 1,56-45;  
 Matches 86; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

DB 1 MEQAPFDGPGPQPEYPPNMTLFLFLFKNEAVHFRFVHSHIQHYETGCTGFWAL 60  
 1 MEQAPFDGPGPQPEYPPNMTLFLFLFKNEAVHFRFVHSHIQHYETGCTGFWAL 60

QY 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96  
 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

DB 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

RESULT 14

Q9E247 PRELIMINARY PRT 96 AA

AC Q9E247

DT 01-MAR-2001 (EMBLrel. 16, created)

DE 01-MAR-2001 (EMBLrel. 16, last sequence update)

DE 01-MAR-2001 (EMBLrel. 16, last annotation update)

DE VPR Protein (FRAGMENT).

GN VPR.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID:11676;

LN 111

RF SEQUENCE FROM N.A.

RC STRAIN:M14.4;

RA Ahmad N., Yedavalli V.S.R.K.;

RT "Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical Transmission."

RI Submitted (09F-2000) to the EMBO/GenBank/TrnB databases.

RI EMBL: AF275120; AAC32278.1;

RI NON-TER 96

FT SEQUENCE 96 AA: 11488 MW: 068DF9C875166810 CRC64:

Query Match 90.7% Score 470; DR 14; Length 96;  
 Best Local Similarity 89.6%; Pred. No. 1,56-45;  
 Matches 86; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

DB 1 MEQAPFDGPGPQPEYPPNMTLFLFLFKNEAVHFRFVHSHIQHYETGCTGFWAL 60  
 1 MEQAPFDGPGPQPEYPPNMTLFLFLFKNEAVHFRFVHSHIQHYETGCTGFWAL 60

QY 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96  
 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

DB 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

QY 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96  
 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

DB 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

RESULT 15

Q9E246 PRELIMINARY PRT 96 AA

AC Q9E246

DT 01-MAR-2001 (EMBLrel. 16, created)

DE 01-MAR-2001 (EMBLrel. 16, last sequence update)

DE 01-MAR-2001 (EMBLrel. 16, last annotation update)

DE VPR Protein (FRAGMENT).

GN VPR.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID:11676;

LN 111

RF SEQUENCE FROM N.A.

RC STRAIN:M14.4;

RA Ahmad N., Yedavalli V.S.R.K.;

RT "Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical Transmission."

RI Submitted (09F-2000) to the EMBO/GenBank/TrnB databases.

RI EMBL: AF275121; AAC32279.1;

RI NON-TER 96

FT SEQUENCE 96 AA: 11488 MW: 068DF9C875166810 CRC64:

Query Match 90.7% Score 470; DR 14; Length 96;  
 Best Local Similarity 89.6%; Pred. No. 1,56-45;  
 Matches 86; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

DB 1 MEQAPFDGPGPQPEYPPNMTLFLFLFKNEAVHFRFVHSHIQHYETGCTGFWAL 60  
 1 MEQAPFDGPGPQPEYPPNMTLFLFLFKNEAVHFRFVHSHIQHYETGCTGFWAL 60

QY 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96  
 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

DB 61 IKLLQQLLFHFRIGRHSRIGIIGRRARRRNSRS 96

Search completed: October 2, 2001, 13:24:26  
 Job time: 184 sec

Wed Oct 3 13:40:06 2001

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Page 6



Example: HIV-1 p24: Enriched.

XX The present invention describes a conjugate composition comprising a  
XX treatment of HIV-1 or non HIV-1 Vpr protein conjugated to a therapeutic  
XX compound. The conjugate can be used in a method for inhibiting cell  
XX proliferation. It can also be used for treating an individual who has a  
XX hyperproliferative disease. The HIV-1 Vpr or non HIV-1 Vpr protein  
XX treatment can be used for identifying compounds that inhibit Vpr protein  
XX binding to the p6 domain of p55 or to p6 protein. The present sequence  
XX represents a HIV protein sequence.

XX Sequence: 96 AA.

Query Match: 100.0%; Score 20; Pos: Length 96  
Best Local Similarity: 100.0%; Pos: No. 276 12;  
Matches: 20; Conservation: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 TWLLELEELKNEAVKHP 20  
111111111111111111  
17 dwtlclclckkncvthlpp 96

RESULT: 2

AAW99815: 100.0%; Score 20; Pos: Length 96

10 AAW99815 standard: protein: 96 AA.

XX AAW99815

XX 09 JUN 1999 (first entry)

XX HIV Vpr Protein sequence: 96

XX HIV Vpr: human immunodeficiency virus; hyperproliferative disease;

XX cell proliferation.

XX Human immunodeficiency virus;

XX W090412-AL

XX 27 FEB 1999

XX 14 AUG 1997: 96W-0518900.

XX 14 AUG 1997: 97NS-0055754.

XX (PDB: ) HIV-1 HENNYVANIA.

XX AAYAG99815: Kibret Lemana T. Michaelian S. Patel M.

XX W090412-AL

XX Conjugate composition comprising HIV-1 Vpr protein treatment - used

XX to inhibit cell proliferation, and treating hyperproliferative

XX disease.

XX Example: HIV-1 p24: Enriched.

XX The present invention describes a conjugate composition comprising a  
XX treatment of HIV-1 or non HIV-1 Vpr protein conjugated to a therapeutic  
XX compound. The conjugate can be used in a method for inhibiting cell  
XX proliferation. It can also be used for treating an individual who has a  
XX hyperproliferative disease. The HIV-1 Vpr or non HIV-1 Vpr protein  
XX treatment can be used for identifying compounds that inhibit Vpr protein  
XX binding to the p6 domain of p55 or to p6 protein. The present sequence  
XX represents a HIV protein sequence.

XX Sequence: 96 AA.

Query Match: 100.0%; Score 20; Pos: Length 96  
Best Local Similarity: 100.0%; Pos: No. 276 12;

Matches: 20; Conservation: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 TWLLELEELKNEAVKHP 20  
111111111111111111  
17 dwtlclclckkncvthlpp 96

RESULT: 4

AAW99812: 100.0%; Score 20; Pos: Length 96

10 AAW99812 standard: protein: 96 AA.

XX AAW99812

XX 09 JUN 1999 (first entry)

XX HIV-1 Vpr protein:

XX HIV Vpr: human immunodeficiency virus; hyperproliferative disease;

XX cell proliferation.

XX Human immunodeficiency virus type 1.

XX W090412-AL

XX 25 FEB 1999

XX 14 AUG 1997: 96W-0518900.

XX 14 AUG 1997: 97NS-0055754.

XX (PDB: ) HIV-1 HENNYVANIA.

XX AAYAG99815: Kibret Lemana T. Michaelian S. Patel M.

XX W090412-AL

XX Conjugate composition comprising HIV-1 Vpr protein treatment - used  
XX to inhibit cell proliferation, and treating hyperproliferative  
XX disease.

XX Example: HIV-1 p24: Enriched.

XX The present invention describes a conjugate composition comprising a  
XX treatment of HIV-1 or non HIV-1 Vpr protein conjugated to a therapeutic  
XX compound. The conjugate can be used in a method for inhibiting cell  
XX proliferation. It can also be used for treating an individual who has a  
XX hyperproliferative disease. The HIV-1 Vpr or non HIV-1 Vpr protein  
XX treatment can be used for identifying compounds that inhibit Vpr protein  
XX binding to the p6 domain of p55 or to p6 protein. The present sequence  
XX represents a HIV-1 Vpr protein sequence.

XX Sequence: 96 AA.

Query Match: 100.0%; Score 20; Pos: Length 96  
Best Local Similarity: 100.0%; Pos: No. 276 12;  
Matches: 20; Conservation: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 TWLLELEELKNEAVKHP 20  
111111111111111111  
17 dwtlclclckkncvthlpp 96

RESULT: 4

AAW99815: 100.0%; Score 20; Pos: Length 96

10 AAW99815 standard: protein: 96 AA.

XX AAW99815

XX 09 JUN 1999 (first entry)

XX HIV Vpr protein sequence.





17. The present invention can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p6 of the p6 protein. The present sequence represents an HIV protein sequence.

18. Sequence: 96 AA.

Query Match: 100.0%; Score: 20; DB: 20; Length: 96;  
 Best Local Similarity: 100.0%; Prod. No. 2,76,12;  
 Matches: 20; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 1 DWPLELEELKNEAVRHPK 20  
 11111111111111111111  
 17 dwpleleelkneavrhpr 36

19. Sequence: 96 AA.  
 AAW99824  
 10 AAW99824 standard; protein: 96 AA.

20. AAW99824

21. Sequence: 96 AA.

22. HIV-1 p6 protein sequence.

23. HIV-1 p6 protein sequence.

24. HIV-1 p6 protein sequence.

25. HIV-1 p6 protein sequence.

26. HIV-1 p6 protein sequence.

27. HIV-1 p6 protein sequence.

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42. HIV-1 p6 protein sequence.

43. HIV-1 p6 protein sequence.

44. HIV-1 p6 protein sequence.

RESULT: 8  
 AAW99824  
 10 AAW99824 standard; protein: 96 AA.

20. AAW99824

21. Sequence: 96 AA.

22. HIV-1 p6 protein sequence.

23. HIV-1 p6 protein sequence.

24. HIV-1 p6 protein sequence.

25. HIV-1 p6 protein sequence.

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53. HIV-1 p6 protein sequence.

54. HIV-1 p6 protein sequence.

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XX 25-FEB-1999
XX
XX 14-AUG-1998; 98WU-0S16890.
XX
XX 14-AUG-1997; 97US-0055754.
XX
XX (DATE ) UNIV PENNSYLVANIA.
XX
XX Agyem V. Kicker-Emmens T. Mahalingam S. Patel M.
XX Weiner DB:
XX
XX WP1: 1999-181154/15.
XX
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX diseases
XX
XX Example: Fig 1B: 64pp; English.
XX
XX
XX The present invention describes a conjugate composition comprising a
XX fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX fragments can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.
XX
XX Sequence 96 AA:
XX
XX Query Match 100.0%; Score 20; E: 20; Length 96;
XX Best Local Similarity 100.0%; Pred. No. 2,76-12;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TWTHLLLELNENAVRHR 20
XX ||||||||||||||||
XX 17 dwtlclclckkroavhrpr 36
XX
XX RESULT 10
XX AAW99825
XX 10 AAW99825 standard: protein: 96 AA.
XX
XX AAW99825.
XX
XX 08-JUN-1999 (first entry)
XX
XX HIV H71V protein sequence.
XX
XX HIV Vpr; human immunodeficiency virus; hyperproliferative disease;
XX cell proliferation.
XX
XX Human immunodeficiency virus.
XX
XX W0999412-A1.
XX
XX 25-FEB-1999.
XX
XX 14-AUG-1998; 98WU-0S16890.
XX
XX 14-AUG-1997; 97US-0055754.
XX
XX (DATE ) UNIV PENNSYLVANIA.
XX
XX Agyem V. Kicker-Emmens T. Mahalingam S. Patel M.
XX Weiner DB:
XX
XX WP1: 1999-181154/15.
XX
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative

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PT diseases
XX
XX Example: Fig 1B: 64pp; English.
XX
XX The present invention describes a conjugate composition comprising a
XX fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX fragments can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.
XX
XX Sequence 96 AA:
XX
XX Query Match 100.0%; Score 20; E: 20; Length 96;
XX Best Local Similarity 100.0%; Pred. No. 2,76-12;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TWTHLLLELNENAVRHR 20
XX ||||||||||||||||
XX 17 dwtlclclckkroavhrpr 36
XX
XX RESULT 11
XX AAW99826
XX 10 AAW99826 standard: protein: 96 AA.
XX
XX AAW99826.
XX
XX 08-JUN-1999 (first entry)
XX
XX HIV G75A protein sequence.
XX
XX HIV Vpr; human immunodeficiency virus; hyperproliferative disease;
XX cell proliferation.
XX
XX Human immunodeficiency virus.
XX
XX W0999412 A1.
XX
XX 25-FEB-1999.
XX
XX 14-AUG-1998; 98WU-0S16890.
XX
XX 14-AUG-1997; 97US-0055754.
XX
XX (DATE ) UNIV PENNSYLVANIA.
XX
XX Agyem V. Kicker-Emmens T. Mahalingam S. Patel M.
XX Weiner DB:
XX
XX WP1: 1999-181154/15.
XX
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX diseases
XX
XX Example: Fig 1B: 64pp; English.
XX
XX The present invention describes a conjugate composition comprising a
XX fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX fragments can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.
XX
XX Sequence 96 AA:

```



WP1: 2960-27044373

XX Expression vector useful for producing infectivity of HIV or for  
XX targeting into HIV virions, comprises nucleic acid segment encoding  
PI recombinant of HIV-1 protein, designated a Vpr/Vpr-vif fusion  
PI incorporation domain.

XX Claim 1: (vif/vpr 210-320): English.

XX The present invention describes an expression vector (1) comprising a  
XX nucleic acid segment encoding a recombinant protein for interfering with  
XX the incorporation of native Vpr/Vpr into HIV-1 or HIV-2 virion, or a  
XX chimeric protein that is incorporated into an HIV-1 or HIV-2 virion,  
XX operably linked to a promoter. Also described are: (1) an isolated  
XX eukaryotic or prokaryotic cell transformed with (1); (2) a composition  
XX for reducing infectivity of HIV-1 or HIV-2 by vitro comprising an  
XX effective amount of (1) in association with a pharmaceutically  
XX acceptable carrier; and (3) a composition for targeting into an HIV-1 or  
XX HIV-2 virion comprising an effective amount of (1) in association with a  
XX pharmaceutically acceptable carrier. (1) has anti-HIV activity and can  
XX be used in gene therapy. (1) is useful for reducing infectivity of HIV  
XX 1: vif/vpr and for targeting into HIV-1 or HIV-2 virion. The present  
XX sequence represents the Vpr protein from HIV, which is used in the  
XX exemplification of the present invention.

XX Sequence 72 AA:

Query Match 95.0% Score 19; Pos 21; Length 72;

Host Local Similarity 100.0% Ident. No. 1; Ref 11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WLELLEELKNEAVRHPPK 20

1111111111111111

10 18 WLELLEELKNEAVRHPPK 46

RESULT 15

AAB69307

11 AAB69307 standard; Protein; 95 AA.

XX AAB69307:

XX 25-APR-2001 (first entry)

XX HIV-1 non-subtype B clone 94CY032-3 vpr protein.

XX HIV-1: human immunodeficiency virus; non-subtype B; gag; pol; env;

XX vpr; vif; vpr; tat; rev; nef; vaccine.

XX Human immunodeficiency virus type 1.

XX W02/0026416-A1.

XX 11-MAY-2001.

XX 25-OCT-1999: 99WO-0824837.

XX 02-NOV-1998: 98US-0184418.

XX (0A88-1) GAG RES. FOUND.

XX Hahn BH, Shaw GM, Gao F;

XX WP1: 2000-05551/31.

XX Novel genomic nucleic acids of non-subtype B human immunodeficiency  
PI virus type 1 useful for detecting and treating AIDS comprises a  
PI specific nucleotide sequence.

XX Claim 41: Fig 17: 14pp; English.

XX The present invention provides the protein and coding sequences for a

XX nucleic acid of human immunodeficiency virus (HIV) type 1 non-subtype B  
XX isolates. The sequences shown include the near full-length coding  
XX sequences from each isolate and the env, pol, tat, vif, vpr, vpr, gag, tat,  
XX rev and nef proteins. These can be used to detect the presence of HIV 1  
XX in a sample and to produce antibodies against non-subtype B HIV-1 virus.  
XX Those antibodies can be used in vaccines to prevent and treat HIV  
XX infection.

XX Sequence 95 AA:

Query Match 95.0% Score 19; Pos 21; Length 95;

Host Local Similarity 100.0% Ident. No. 2; Ref 11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WLELLEELKNEAVRHPPK 20

1111111111111111

10 18 WLELLEELKNEAVRHPPK 46

Search completed: 09/09/01 13:25:20  
Job time: 188 sec

Wed Oct 3 13:40:06 2001

us-09-485-421-1\_copy\_17\_36.rag

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Page 8

GenCore version 4.5  
Copyright (c) 1999 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2001, 13:23:42, Search time 18.81 seconds  
(without alignments)  
21,893 Million cell updates/sec

Title: US-09-485-421-1\_COPY\_17\_36

Percent: 96

Sequence: 1 DMTLLEIKRKNVNIIFR 20

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 197339 seqs, 20590346 residues

Word size: 0

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 290000000

Post processing: listing first 45 summaries

Database: Issued\_Patents\_AA \*

1: /usr/local/ncbi/blast/seq/seq\_5A\_G0M3.pat.\*  
2: /usr/local/ncbi/blast/seq/seq\_5A\_G0M3.pat.\*  
3: /usr/local/ncbi/blast/seq/seq\_5A\_G0M3.pat.\*  
4: /usr/local/ncbi/blast/seq/seq\_5A\_G0M3.pat.\*  
5: /usr/local/ncbi/blast/seq/seq\_5A\_G0M3.pat.\*  
6: /usr/local/ncbi/blast/seq/seq\_5A\_G0M3.pat.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	19	95.0	72 2 US-08-301-915-4	Sequence 4, App1
2	19	95.0	72 3 US-08-334-631A-1	Sequence 4, App1
3	19	95.0	78 4 US-09-124-900-5	Sequence 5, App1
4	19	95.0	96 7 US-08-501-915-1	Sequence 1, App1
5	19	95.0	96 3 US-08-524-694A-1	Sequence 1, App1
6	10	50.0	96 3 US-08-704-8560-15	Sequence 15, App
7	8	40.0	18 3 US-08-940-095-196	Sequence 196, App
8	8	40.0	18 3 US-08-940-095-196	Sequence 196, App
9	9	40.0	18 3 US-08-940-095-196	Sequence 196, App
10	7	35.0	16 3 US-08-940-095-253	Sequence 253, App
11	7	35.0	16 3 US-08-940-093-253	Sequence 253, App
12	7	35.0	16 3 US-08-940-096-253	Sequence 253, App
13	7	35.0	18 3 US-08-940-095-192	Sequence 191, App
14	7	35.0	18 3 US-08-940-095-192	Sequence 192, App
15	7	35.0	18 3 US-08-940-095-194	Sequence 193, App
16	7	35.0	18 3 US-08-940-095-194	Sequence 194, App
17	7	35.0	18 3 US-08-940-095-195	Sequence 195, App
18	7	35.0	18 3 US-08-940-095-197	Sequence 197, App
19	7	35.0	18 3 US-08-940-095-198	Sequence 198, App
20	7	35.0	18 3 US-08-940-095-200	Sequence 200, App
21	7	35.0	18 3 US-08-940-095-201	Sequence 201, App
22	7	35.0	18 3 US-08-940-095-203	Sequence 203, App
23	7	35.0	18 3 US-08-940-095-204	Sequence 204, App
24	7	35.0	18 3 US-08-940-095-206	Sequence 206, App
25	7	35.0	18 3 US-08-940-095-207	Sequence 207, App
26	7	35.0	18 3 US-08-940-095-210	Sequence 210, App
27	7	35.0	18 3 US-08-940-095-214	Sequence 214, App

28	7	35.0	18 3 US-08-940-095-216	Sequence 216, App
29	7	35.0	18 3 US-08-940-095-221	Sequence 221, App
30	7	35.0	18 3 US-08-940-095-231	Sequence 231, App
31	7	35.0	18 3 US-08-940-093-191	Sequence 191, App
32	7	35.0	18 3 US-08-940-093-192	Sequence 192, App
33	7	35.0	18 3 US-08-940-093-193	Sequence 193, App
34	7	35.0	18 3 US-08-940-093-194	Sequence 194, App
35	7	35.0	18 3 US-08-940-093-195	Sequence 195, App
36	7	35.0	18 3 US-08-940-093-197	Sequence 197, App
37	7	35.0	18 3 US-08-940-093-198	Sequence 198, App
38	7	35.0	18 3 US-08-940-093-200	Sequence 200, App
39	7	35.0	18 3 US-08-940-093-201	Sequence 201, App
40	7	35.0	18 3 US-08-940-093-203	Sequence 203, App
41	7	35.0	18 3 US-08-940-093-204	Sequence 204, App
42	7	35.0	18 3 US-08-940-093-206	Sequence 206, App
43	7	35.0	18 3 US-08-940-093-207	Sequence 207, App
44	7	35.0	18 3 US-08-940-093-210	Sequence 210, App
45	7	35.0	18 3 US-08-940-093-214	Sequence 214, App

#### ALIGNMENTS

##### RESULT 1

US-08-301-915-4  
Sequence 4, Application US/08301915

Patent No. 5861161

##### GENERAL INFORMATION:

APPLICANT: COHEN, ERIC A.

APPLICANT: BERGERON, Dominique

APPLICANT: CHEPPE, Florent

APPLICANT: YAO, Xiao-Tian

APPLICANT: FERNANDEZ, JEFFREY, JEFFREY

TITLE: INVENTION FOR THE IDENTIFICATION OF HIV-1 VIRUS

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TITLE: INVENTION FOR THE IDENTIFICATION OF HIV-1 VIRUS

TITLE: INVENTION FOR THE IDENTIFICATION OF HIV-1 VIRUS

Query Match: 95.0%, Score: 19, DB: 2, Length: 72  
Percent similarity: 100.0%, Pred. No. 26-116  
Matches: 19, Conservation: 0, Mismatches: 0, Gaps: 0





US-08-403-915-1

Query Match 95.0%; Score 19; DR 2; Length 96;  
 Best Local Similarity 100.0%; Prod. No. 2,56-11;  
 Matches 19; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WTELELEKRAVHEHTP 29  
 18 WTELELEKRAVHEHTP 36

RESULT 5  
 US-08-524-694A-1

Sequence 1, Application US/08/524694A  
 Patent No. 6043081  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, LITE A.  
 APPLICANT: BEISLER, Florence  
 APPLICANT: CHURCH, Florence  
 APPLICANT: VA, CDC, JPL  
 APPLICANT: FICHAS KONIGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED  
 TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: KLAUSER & JACKSON  
 STREET: Continental Plaza, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: N.J.  
 ZIP: 07601  
 COUNTRY: U.S.A.  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/08/524,694A  
 FILING DATE: September 7, 1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT: ZNEBMA7714  
 NAME: JACKSON, David A.  
 REGISTRATION NUMBER: 26,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5809  
 TELEFAX: 201-443-1684  
 TELETYPE: 145721  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 STRANDNESS: single  
 TOPOLOGY: linear  
 M-REUSE TYPE: protein  
 HYPOTHETICAL: NO  
 US-08-524-694A-1

Query Match 95.0%; Score 19; DR 4; Length 96;  
 Best Local Similarity 100.0%; Prod. No. 2,56-11;  
 Matches 19; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WTELELEKRAVHEHTP 29  
 18 WTELELEKRAVHEHTP 36

RESULT 6  
 US-08-704-8560-15  
 Sequence 15, Application US/08/7048560  
 Patent No. 6042842  
 GENERAL INFORMATION:

APPLICANT: Kufrowski, Hilary  
 APPLICANT: Yusibov, Vidadi  
 APPLICANT: Hooper, Douglas, C.  
 APPLICANT: Madelska, Anna  
 TITLE OF INVENTION: Polypeptides fused with Plant Virus  
 TITLE OF INVENTION: Coat Proteins  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Allan H. Fiedel & Associates  
 STREET: 1525 Locust Street, 15th floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: USA  
 ZIP: 19102

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS DOS  
 SOFTWARE: Corel WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/08/704,8560  
 FILING DATE: 28-Aug-1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fiedel, Allan H.  
 REGISTRATION NUMBER: 41,253  
 REFERENCE/EXCERPT NUMBER: 119-007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 732-7090  
 TELEFAX: (215) 732-7090  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 HYPOTHETICAL: N  
 US-08-704-8560-15

Query Match 50.0%; Score 10; DR 3; Length 96;  
 Best Local Similarity 100.0%; Prod. No. 0,0057;  
 Matches 19; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WTELELEKRAVHEHTP 29  
 18 WTELELEKRAVHEHTP 36

RESULT 7  
 US-08-940-095-196  
 Sequence 196, Application US/08/940095  
 Patent No. 6004925  
 GENERAL INFORMATION:  
 APPLICANT: Hossain, Jean-Louis  
 APPLICANT: Sekul, Renata  
 APPLICANT: Butner, Klaus  
 APPLICANT: Cornuti, Isabelle  
 APPLICANT: Metz, Gerd  
 APPLICANT: Hoffmeyer, Jean  
 TITLE OF INVENTION: ANTIFERTILIN A-1 AGONISTS  
 TITLE OF INVENTION: AND THEIR USE TO TREAT EPIDIDYMIC DISORDERS  
 NUMBER OF SEQUENCES: 298  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fongle & Edwards LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036-2811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS

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1  NAME: CORRUPT, Laura A
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: 009196-0006-999
4  FILING DATE: 29 SEP 1997
5  CLASSIFICATION: 911
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER:
8  FILING DATE:
9  ATTORNEY/AGENT INFORMATION:
10 NAME: CORRUPT, Laura A
11 REGISTRATION NUMBER: 40,742
12 REFERENCE/ISSUE NUMBER: 009196-0006-999
13 CLASSIFICATION INFORMATION:
14 TELEPHONE: 650-493-4945
15 TELEFAX: 650-493-4945
16 TELE: 66141 PENNIE
17 INFORMATION FOR SEQ ID NO: 196:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 18 amino acids
20 TYPE: amino acid
21 STANDARDS: single
22 MOLECULE TYPE: protein
23 FEATURES:
24 NAME/KEY: other
25 LOCATION: 1-18
26 OTHER INFORMATION: N terminal acetylated and
27 OTHER INFORMATION: C terminal unaltered
28 US-09-485-421-1

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07 5 ELITEK 1.2
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1  NAME: CORRUPT, Laura A
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: 009196-0006-999
4  FILING DATE: 29 SEP 1997
5  CLASSIFICATION: 911
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER:
8  FILING DATE:
9  ATTORNEY/AGENT INFORMATION:
10 NAME: CORRUPT, Laura A
11 REGISTRATION NUMBER: 40,742
12 REFERENCE/ISSUE NUMBER: 009196-0006-999
13 CLASSIFICATION INFORMATION:
14 TELEPHONE: 650-493-4945
15 TELEFAX: 650-493-4945
16 TELE: 66141 PENNIE
17 INFORMATION FOR SEQ ID NO: 196:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 18 amino acids
20 TYPE: amino acid
21 STANDARDS: single
22 MOLECULE TYPE: protein
23 FEATURES:
24 NAME/KEY: other
25 LOCATION: 1-18
26 OTHER INFORMATION: N terminal acetylated and
27 OTHER INFORMATION: C terminal unaltered
28 US-09-485-421-1

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1  NAME: CORRUPT, Laura A
2  REGISTRATION NUMBER: 40,742
3  REFERENCE/ISSUE NUMBER: 009196-0006-999
4  TELEPHONE: 650-493-4945
5  TELEFAX: 650-493-4945
6  TELE: 66141 PENNIE
7  INFORMATION FOR SEQ ID NO: 196:
8  SEQUENCE CHARACTERISTICS:
9  LENGTH: 18 amino acids
10 TYPE: amino acid
11 STANDARDS: single
12 MOLECULE TYPE: protein
13 FEATURES:
14 NAME/KEY: other
15 LOCATION: 1-18
16 OTHER INFORMATION: N terminal acetylated and
17 OTHER INFORMATION: C terminal unaltered
18 US-09-485-421-1

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99 111111
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```

1  NAME: CORRUPT, Laura A
2  REGISTRATION NUMBER: 40,742
3  REFERENCE/ISSUE NUMBER: 009196-0006-999
4  TELEPHONE: 650-493-4945
5  TELEFAX: 650-493-4945
6  TELE: 66141 PENNIE
7  INFORMATION FOR SEQ ID NO: 196:
8  SEQUENCE CHARACTERISTICS:
9  LENGTH: 18 amino acids
10 TYPE: amino acid
11 STANDARDS: single
12 MOLECULE TYPE: protein
13 FEATURES:
14 NAME/KEY: other
15 LOCATION: 1-18
16 OTHER INFORMATION: N terminal acetylated and
17 OTHER INFORMATION: C terminal unaltered
18 US-09-485-421-1

```

```

1 LENGTH: 18 amino acids
2 TYPE: amino acid
3 STRANDEDNESS: single
4 TOPOLOGY: linear
5 MOLECULE TYPE: No. 60461666
6 PVALUUP:
7
8 NAME: 18
9 IDENTIFICATION: N-terminal acetylated and
10 OTHER IDENTIFICATION: C-terminal amidated
11
12 MS-008-040-0-066-1396

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Quality Match	40.0%	Score B:	DN 4:	Length 18:	
Post-Join Similarity	100.0%	Prod. No. 0.1:			
Matches	8	Mismatches	0	Totals	n: 8
5 ELEPHANT 12					
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10b 8 ELEPHANT 15					

RESULT 10  
 US-08-440-095-251  
 Sequence 250 Affiliation: 0098649095  
 Patent No: 6004925  
 GENERAL INFORMATION:  
 APPLICANT: Dasseux, Jean-Louis  
 APPLICANT: Sokol, Renate  
 APPLICANT: Fortnot, Klaus  
 APPLICANT: Cornuet, Isabelle  
 APPLICANT: Melzi, Guiller  
 APPLICANT: Dailourcy, Jean  
 TITLE OF INVENTION: Aminoacetic A-1 AMINIDES  
 TITLE OF INVENTION, AND THEIR USE TO TREAT ENOSTIOTIC DISEASES  
 NUMBER OF SEQUENCES: 258  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Parnis & Edmunds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036-2811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 M-METHOD: IBM Compatible  
 OPERATING SYSTEM: VMS  
 SOFTWARE: FASTSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 FILING DATE: 29-SEP-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING NAME:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cornuet, Louis A  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/AGENT NUMBER: 00956-001-009  
 TELEPHONE: 650-493-4935  
 TELEFAX: 650-493-5556  
 TELE: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 251:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: linear  
 PEATRE:  
 NAME/KEY: 4500  
 LOCATION: 1...16

OTHER INFORMATION: N-terminal acetylated and  
OTHER INFORMATION: C-terminal amidated  
US-08-940-095-253

Query Match:	25/100	Score 71	DB 3	Length 16
Percent Identity:	100.00	Field No. 0072		
Matches:	7	Conservation	0	Mismatches
			0	Indels
			0	Gaps
QY	5	ELLEBK	11	
DB	8	ELLEBK	14	

RESULT 11  
US-08-940-0943-253  
Sequence: 253, Application: US/0894009-  
Patent No. 6037323  
GENERAL INFORMATION:  
APPLICANT: Dassault, Jean-Louis  
APPLICANT: Sekul, Ronald  
APPLICANT: Butler, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
TITLE OF INVENTION: A METHOD FOR THE TREATMENT OF ALLERGIC REACTIONS AND THEIR USE TO TREAT EXALTIHERMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ronnic & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPILED BY: RALPH FORMER  
MEDIUM TYPE: diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
At 11:23:13.48 on 08/26/97, 08/26/940, 093  
FILING DATE: 29-SEP-1997  
CLASSIFICATION: A35  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, Laura A  
REGISTRATION NUMBER: 39,742  
E-mail address: lcoruzzi@att.net  
TELEPHONE: 650-493-4945  
TELEFAX: 650 493-5556  
FACSIMILE: 60141 PHOENIX  
INFORMATION PER SEQ ID NO: 253:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STEPWISES: single  
TAG TAG: linear  
MULTIPLE TYPE: NO, 60373236  
FEATURES:  
NAME/KEY: other  
LOCATION: 1...16  
OTHER INFORMATION: N-terminal acetylated and  
OTHER INFORMATION: C-terminal amidated  
US-08-940-0943-253

Quality Match 35.08; Score 7; Ed 3; Length 16;  
Best Local Similarity 100.0%; Prod. No. 0.76;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

57 5 FILEBK 11  
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140 8 FILEBK 11

RESULT 14  
US-09-940-095-258

Sequence 14: Application US-09-940-095-258  
Patent No. 604106

GENERAL INFORMATION:

APPLICANT: Dassou, Jean-Louis

APPLICANT: Social, Katus

APPLICANT: Buttet, Klaus

APPLICANT: Court, Isabelle

APPLICANT: Metz, Gunter

TITLE OF INVENTION: APOLYPROTEIN A-1 ANALYSTS

NUMBER OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

ADDRESSSEE: Ponto & Edwards LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10046-2011

COMPUTER RELEVABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSP Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-940-095-258

FILING DATE: 29 SEP 1997

CLASSIFICATION: G06

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Court, Laura A

REGISTRATION NUMBER: 40,742

REFERENCE/PACKET NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650 493 4935

TELEFAX: 650 493 5556

TELEX: 66141 PENNIE

INFORMATION FOR SPO TO NO: 191:

SPECIFIC CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

MODULO TYPE: No. 60049250

FEATURE:

NAME/KEY: other

LOCATION: 1...18

OTHER INFORMATION: N-terminal acetylated and

OTHER INFORMATION: C-terminal amidated

US-09-940-095-258

Query Match: 5.0%, Score 71, 100%, Length 187

Best Local Similarity: 100.0%, Prod. No. 0.0%

Matches: 71, conservative 0, Mismatch 0, Indels 0, Gaps 0

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8 FILEBK 11

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GENERAL INFORMATION:

APPLICANT: Dassou, Jean-Louis

APPLICANT: Social, Katus

APPLICANT: Buttet, Klaus

APPLICANT: Court, Isabelle

APPLICANT: Metz, Gunter

TITLE OF INVENTION: APOLYPROTEIN A-1 ANALYSTS

NUMBER OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

ADDRESSSEE: Ponto & Edwards LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10046-2011

COMPUTER RELEVABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSP Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09-940-095-258

FILING DATE: 29 SEP 1997

CLASSIFICATION: G14

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Court, Laura A

REGISTRATION NUMBER: 40,742

REFERENCE/PACKET NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650 493 4935

TELEFAX: 650 493 5556

TELEX: 66141 PENNIE

INFORMATION FOR SPO TO NO: 191:

SPECIFIC CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

MODULO TYPE: No. 60049250

FEATURE:

NAME/KEY: other

LOCATION: 1...18

OTHER INFORMATION: N-terminal acetylated and

OTHER INFORMATION: C-terminal amidated

US-09-940-095-191

Query Match: 5.0%, Score 71, 100%, Length 187

Best Local Similarity: 100.0%, Prod. No. 0.0%

Matches: 71, conservative 0, Mismatch 0, Indels 0, Gaps 0

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8 FILEBK 14

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1 TITLE OF INVENTION: ANTIBIOTIC USE TO TREAT ESCHERICHIA COLI INFECTIONS  
 2 NUMBER OF SEQUENCES: 258  
 3 CORRESPONDENCE ADDRESS:  
 4 ADDRESSEE: Penzo & Edmonds LLP  
 5 STREET: 1155 Avenue of the Americas  
 6 CITY: New York  
 7 STATE: NY  
 8 COUNTRY: USA  
 9 FILING DATE: 1004-2811  
 10 COMPUTER READABLE FORM:  
 11 MEDIUM TYPE: diskette  
 12 COMPUTER: IBM compatible  
 13 OPERATING SYSTEM: DOS  
 14 SOFTWARE: FASTSEQ Version 2.0  
 15 CURRENT APPLICATION DATA:  
 16 APPLICATION NUMBER: 09/094,095  
 17 FILING DATE: 29-SEP-1997  
 18 CLASSIFICATION: 514  
 19 PRIORITY APPLICATION DATA:  
 20 APPLICATION NUMBER:  
 21 FILING DATE:  
 22 ATTORNEY/AGENT INFORMATION:  
 23 NAME: Cornuzzi, Laura A  
 24 REGISTRATION NUMBER: 30,742  
 25 REFERENCE/EXCERPT NUMBER: 09/106,094-999  
 26 TELECOMMUNICATION INFORMATION:  
 27 TELEPHONE: 650-493-4935  
 28 TELEFAX: 650-493-5556  
 29 INDEX: 66141 PENNIE  
 30 INFORMATION FOR SEQ ID NO: 192:  
 31 SEQUENCE CHARACTERISTICS:  
 32 LENGTH: 18 amino acids  
 33 TYPE: amino acid  
 34 STRANDEDNESS: single  
 35 TOPOLOGY: linear  
 36 MOLECULAR TYPE: NO: 60049250  
 37 FEATURE:  
 38 NAME/KEY: other  
 39 LOCATION: 1...18  
 40 OTHER INFORMATION: N-terminal acetylated and  
 41 OTHER INFORMATION: C-terminal amidated  
 42 US-08-940-095-192  
 43  
 44 Query Match 35.0% Score 72 DB 31 Length 18:  
 45 Best Local Similarity: 100.0%, Pval: No. 0.85;  
 46 Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
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 48 QY 5 ELLEFLK 11  
 49 DB 8 ELLEFLK 14  
 50  
 51 RESULT 15  
 52 US-08-940-095-193  
 53 Sequence 193, Application US/08940095  
 54 Patent No. 6004925  
 55 GENERAL INFORMATION:  
 56 APPLICANT: Lassoux, Jean-Louis  
 57 APPLICANT: Sekul, Renate  
 58 APPLICANT: Buttner, Klaus  
 59 APPLICANT: Cornut, Isabelle  
 60 APPLICANT: Metz, Guinter  
 61 APPLICANT: Buiourey, Jean  
 62 TITLE OF INVENTION: APOLIPOPROTEIN A-1 ANAGONISTS  
 63 TITLE OF INVENTION: AND THEIR USE TO TREAT HYSLIPIDEMIC DISORDERS  
 64 NUMBER OF SEQUENCES: 258  
 65 CORRESPONDENCE ADDRESS:  
 66 ADDRESSEE: Penzo & Edmonds LLP  
 67 STREET: 1155 Avenue of the Americas  
 68 CITY: New York  
 69 STATE: NY  
 70 COUNTRY: USA

1 ZIP: 10046-2811  
 2 COMPUTER READABLE FORM:  
 3 MEDIUM TYPE: diskette  
 4 COMPUTER: IBM compatible  
 5 OPERATING SYSTEM: DOS  
 6 SOFTWARE: FASTSEQ Version 2.0  
 7 CURRENT APPLICATION DATA:  
 8 APPLICATION NUMBER: 09/094,095  
 9 FILING DATE: 29-SEP-1997  
 10 CLASSIFICATION: 514  
 11 PRIORITY APPLICATION DATA:  
 12 APPLICATION NUMBER:  
 13 FILING DATE:  
 14 ATTORNEY/AGENT INFORMATION:  
 15 NAME: Cornuzzi, Laura A  
 16 REGISTRATION NUMBER: 30,742  
 17 REFERENCE/EXCERPT NUMBER: 09/106,094-999  
 18 TELECOMMUNICATION INFORMATION:  
 19 TELEPHONE: 650-493-4935  
 20 TELEFAX: 650-493-5556  
 21 INDEX: 66141 PENNIE  
 22 INFORMATION FOR SEQ ID NO: 193:  
 23 SEQUENCE CHARACTERISTICS:  
 24 LENGTH: 18 amino acids  
 25 TYPE: amino acid  
 26 STRANDEDNESS: single  
 27 TOPOLOGY: linear  
 28 MOLECULAR TYPE: NO: 60049250  
 29 FEATURE:  
 30 NAME/KEY: other  
 31 LOCATION: 1...18  
 32 OTHER INFORMATION: N-terminal acetylated and  
 33 OTHER INFORMATION: C-terminal amidated  
 34 US-08-940-095-193  
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 36 Query Match 45.0% Score 72 DB 31 Length 18:  
 37 Best Local Similarity: 100.0%, Pval: No. 0.85;  
 38 Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 39  
 40 QY 5 ELLEFLK 11  
 41 DB 8 ELLEFLK 14  
 42  
 43 Search completed: October 2, 2001, 17:27:46  
 44 Job Time: 124 sec





best local similarity 100.0% Score 102.1982 Length 962  
Matches 142 Conservative 02 Mismatch 02 Indels 02 Gaps 02

Query 1 UFEKNEAVRHR 20  
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100 UFEKNEAVRHR 20

RESULT 4  
1.000

Query Protein human immunodeficiency virus type 1 (isolate cat1.1)  
Species: human immunodeficiency virus type 1, HIV-1

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Date: 11 Jun 1993  
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submitted to the EMBL Data Library, July 1989  
Accession number: S54867

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Wed Oct 3 13:40:07 2001

us-09-485-421-1\_copy\_17\_36.rpr

Page 5

Search completed: October 3, 2001, 13:29:03  
Job time: 271 sec

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DT	01-OCT-2000 (IEMBL01, 15, Last sequence update)
FE	01-MAR-2001 (IEMBL01, 15, Last annotation update)
DE	VPE, PROTEIN.
GN	VPE.
OS	Human immunodeficiency virus type 1.
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID:11476;
RA	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
SC	STEININ-PATENT 18;
EX	MEPLIN-20348/96; PubMed 1081687;
KA	Yamada T., Iwamoto A.;
RT	"Comparison of proviral accessory genes between long-term
RI	nonprogressors and progressors of human immunodeficiency virus type 1
RI	infection.";
RL	Arch. Virol. 145:1021-1027(2000).
DR	EMBL; AB034554; AAA94001.1; -;
DR	IntePro; IP0000012; -;
DR	IntePro; IP001594; -;
DR	PIfam; PF005522; VPE; 1.
DR	PRINTS; PR00444; HIVVPRVX.
DR	Proteome; IP001667; -; 1.
NU	SEQUENCE 96 AA; 11306 MW; 407137E53042F0; CDS64;

	Query Match:	100.0%	Score 20	Pos 14	Length 96;
	Best Local Similarity:	100.0%	Freq. No. 7	5e-11;	
	Matches 20	Conservative	0	Mismatches 0	Indels 0; Gaps 0;
OY	1 DWTLEELKEHKNCAVRPPR	20			
D8	17 DWTLEELKEHKNCAVRPPR	36			
RESULT	5				
Q89598					
ID	Q89598	PROTEINIMINARY:	PRT:	47 AA.	
AC	Q89598:				
DT	01-NOV-1996 (JTEMBLrefl_01_Created)				
D1	01-NOV-1996 (JTEMBLrefl_01_Last sequence update)				
D3	01-MAY-2000 (JTEMBLrefl_13_Last annotation update)				
DE	HIV-1 DNA POL CAG, POL, VIF, VIK, VRX, TAT, ENV, VP1,				
NM	VPR.				
OS	Human immunodeficiency virus type 1.				
GC	Retroviruses, betroid viruses, retroviridae; Lentiviruses.				
OX	NCBI TaxId: 11676;				
RN	[1]				
KC	SEQUENCE FROM N.A.				
SC	STRAIN=EMZ13;				
RA	Cloyd M.W., Moore B.E.;				
KL	Submitted (Jun 1996) to the EMBL/Genbank/JFRL databases.				
LN	[2]				
RP	SEQUENCE FROM N.A.				
SC	STRAIN=EMZ13;				
RA	Matodi V.;				
KL	Submitted (Aug 1995) to the EMBL/Genbank/JFRL databases.				
DR	EMBL: D86069; PAAI2999.1;				
DR	EMBL: D86069; PAAI2991.1;				
DR	InterPro: IPR00012;				
DR	Tram: PR00522; Virg: 1.				
CC	FUNCTION: 47 AA; 448 MG; 410700049735277 cto64;				

Query Match	95.08	Score 19	Eth 14	Length 37
Best Local Similarity	100.08	Prod. No. 2	Yes-10	
Matches	19	Conservative	0	Mismatches 0
			0	Gaps 0

2 WTELELEKNAVHPR 20  
 16 18 WTELELEKNAVHPR 36

## RESULT 6

0796107 PRELIMINARY: PRI: 67 AA.

AC 0796107:

01 01-NOV-1999 (TREMblrel\_12, Created)

02 01-NOV-1999 (TREMblrel\_12, Last sequence update)

03 01-MAR-2000 (TREMblrel\_16, Last annotation update)

04 VPR PROTEIN (FRAGMENT).

05 VPR.

06 Human immunodeficiency virus type 1.

07 Viruses; Retroviral viruses; Retroviridae; Lentivirus.

08 NCBI\_TaxID=11676;

09 [1]

10 SEQUENCE FROM N.A.

11 STRAIN:INFANT PATR A.

12 MIMIC: 0822222; PubMed 065910.

13 Yedavalli V.R., Chappey C., Ahmad N.

14 "Mitigation of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission."

15 J. Virol. 72:6937-6943(1998)

16 EMBL: AF042894; AAC41064.1;

17 InterPro: IPR000912; -

18 Pfam: PF00522; VPR.1

19 PRINTS: PR00444; HIVPRVFX.

20 NON\_TER 67

21 SEQUENCE: 67 AA: 7930 MW: 5081866139730E C6064.

2 WTELELEKNAVHPR 20  
 18 WTELELEKNAVHPR 36

## RESULT 7

090667 PRELIMINARY: PRI: 93 AA.

AC 090667:

01 01-MAY-2000 (TREMblrel\_13, Created)

02 01-MAY-2000 (TREMblrel\_13, Last sequence update)

03 01-MAR-2000 (TREMblrel\_16, Last annotation update)

04 VPR PROTEIN.

05 VPR.

06 Human immunodeficiency virus type 1.

07 Viruses; Retroviral viruses; Retroviridae; Lentivirus.

08 NCBI\_TaxID=11676;

09 [1]

10 SEQUENCE FROM N.A.

11 STRAIN:96F4071;

12 Anderson J.P., Rodrigo A.G., Igarashi H., Madan A., Delabroy C.

13 "Gao M., Girard M., Osmanov S., Hoed L., Mullins J.L.

14 "Testing the hypothesis of a recombinant origin of human

15 immunodeficiency virus type 1 subtype B."

16 Submitted (OCT-1999) to the EMBL/GenBank/CCDB databases.

17 EMBL: AF197341; AAC24336.1;

18 InterPro: IPR00012; -

19 Pfam: PF00522; VPR.1

20 PRINTS: PR00444; HIVPRVFX.

21 SEQUENCE: 93 AA: 11151 MW: 8A299EAB2CA2ACB C6064;

2 WTELELEKNAVHPR 20  
 18 WTELELEKNAVHPR 36

## RESULT 8

079253 PRELIMINARY: PRI: 94 AA.

AC 079253:

01 01-NOV-1996 (TREMblrel\_01, Created)

02 01-NOV-1996 (TREMblrel\_01, Last sequence update)

03 01-MAY-2000 (TREMblrel\_13, Last annotation update)

04 VPR PROTEIN.

05 VPR.

06 Human immunodeficiency virus type 1.

07 Viruses; Retroviral viruses; Retroviridae; Lentivirus.

08 NCBI\_TaxID=11676;

09 [1]

10 SEQUENCE FROM N.A.

11 STRAIN:INFANT:467; IFMOSFVAL; GERMANY

12 Farkas E., Gabor J., Gabor J., Gabor J., Hartman S., Gibbs J.

13 Goudant J.

14 J. Gen. Virol. 69:0-0(1996).

15 EMBL: Z68557; CAA92881.1;

16 InterPro: IPR00012; -

17 Pfam: PF00522; VPR.1

18 PRINTS: PR00444; HIVPRVFX.

19 SEQUENCE: 94 AA: 11150 MW: 8A299EAB2CA2ACB C6064;

2 WTELELEKNAVHPR 20  
 18 WTELELEKNAVHPR 36

## RESULT 9

P88158 PRELIMINARY: PRI: 94 AA.

AC P88158:

01 01-MAY-1997 (TREMblrel\_03, Created)

02 01-MAY-1997 (TREMblrel\_03, Last sequence update)

03 01-MAY-2000 (TREMblrel\_13, Last annotation update)

04 VPR PROTEIN.

05 VPR.

06 Human immunodeficiency virus type 1.

07 Viruses; Retroviral viruses; Retroviridae; Lentivirus.

08 NCBI\_TaxID=11676;

09 [1]

10 SEQUENCE FROM N.A.

11 Gao F., Robertson D.L., Morrison S.G., Hui H., Craig S., Fultz P.N.

12 Decker J., Girard M., Shaw G.M., Hahn B.H., Sharp P.M.

13 J. Virol. 0:0-0(0).

14 [12]

15 SEQUENCE FROM N.A.

16 Gao F., Robertson D.L., Morrison S.G., Hui H., Craig S., Fultz P.N.

17 Decker J., Girard M., Shaw G.M., Hahn B.H., Sharp P.M.

18 Submitted (MAR-1996) to the EMBL/GenBank/CCDB databases.

19 EMBL: U51189; AAB38835.1;

20 InterPro: IPR00012; -

21 Pfam: PF00522; VPR.1

22 PRINTS: PR00444; HIVPRVFX.

23 SEQUENCE: 94 AA: 11384 MW: C0990AB909C2E03 C6064;

Query Match: 95.0%; Score 19; DB 14; Length 94;  
 Best Local Similarity: 100.0%; Prod. No. 5,6e-10;  
 Matches: 19; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 2 WTELELEKNAVHPR 20





11 01-NOV-1996 (TREMUREL\_01, last sequence update)  
 10 01-MAY-2000 (TREMUREL\_13, last annotation update)  
 09 VPR PROTEIN.  
 08 Human immunodeficiency virus type 1.  
 07 Viruses: Retroviridae: Retroviridae: Lentivirus.  
 06 NCBI\_taxid:11676.  
 05 [1]  
 04 SEQUENCE FROM N.A.  
 03 STRAIN PATENT: 7025, IV PROG USER, DUTCH  
 02 KUIKOR L., GERMELISSEN E., ZORDRAGER F., HARTMAN S., GIBBS J.,  
 01 Goudsmit J.;  
 00 J. Gen. Virol. 0:0-0(1996).  
 99 EMBL: Z68583; CAA92907.1; .  
 98 InterPro: IPR00012; .  
 97 Pfam: PF00522; VPR\_1.  
 96 PRINTS: PR00444; HIVPRVPR.  
 95 SEQUENCE 95 AA: 11278 MW: 842219.624 GC64;

## Query Match

Score 19; DB 14; Length 95;

Best Local Similarity 100.0%; Pred. No. 5,7e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WTLLEELKKNFAVHHPK 20  
 10 WTLLEELKKNFAVHHPK 35

RESULT 15  
 ID 097061 FRILIMARY; PRI: 95 AA.  
 AC 097061;

01-FEB-1997 (TREMUREL\_02, created)  
 01-FEB-1997 (TREMUREL\_02, last sequence update)  
 01-MAY-2000 (TREMUREL\_13, last annotation update)  
 04 STRAIN CM240, COMPLETE PROVIRAL GENOME.  
 03 VPR.  
 02 Human immunodeficiency virus type 1.  
 01 Viruses: Retroviridae: Retroviridae: Lentivirus.  
 00 NCBI\_taxid:11676.  
 99 [1]  
 98 SEQUENCE FROM N.A.  
 97 MERLINE 95323197; PUBMED-8799215;  
 96 GART J.K., SALMON M.O., KOCH G., GORTE D., ARNSTEIN A.W.,  
 95 HENRICH E.A., LAUS D., BURKE D.S., MCCUTCHAN F.E.;  
 94 4Full-length sequence and mosaic structure of a human immunodeficiency  
 93 virus type 1 isolate from Thailand.  
 92 J. Virol. 70:5935-5941(1996).  
 91 EMBL: U54771; AAC5462.1; .  
 90 InterPro: IPR00012; .  
 89 Pfam: PF00522; VPR\_1.  
 88 PRINTS: PR00444; HIVPRVPR.  
 87 SEQUENCE 95 AA: 11168 MW: 481EF2928798CF GC64;

## Query Match

Score 19; DB 14; Length 95;

Best Local Similarity 100.0%; Pred. No. 5,7e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WTLLEELKKNFAVHHPK 20  
 10 WTLLEELKKNFAVHHPK 35

Search completed: October 3, 2001, 13:30:12  
 Job time: 290 sec





Example: Fig 1b: 64pp: English.

the present invention describes a conjugate composition comprising a fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic compound. The conjugate can be used in a method for inhibiting cell proliferation. It can also be used for treating an individual who has a hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein fragments can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents an HIV protein sequence.

Sequence: 96 AA:

Query Match: 100.0%; Score: 26; DB: 20; Length: 96;  
 Best Local Similarity: 100.0%; Pred. No. 8, 26-19;  
 Matches: 26; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 ALKRLDQQLFHFRRGCRSRGII 26  
 59 a1111q1111h1h1h1h1h1h1 84

RESULT: 2

AAW99815: 100.0%; Score: 26; DB: 20; Length: 96;  
 ID: AAW99815 standard: protein; 96 AA.

AAW99815:

08-JUN-1999 (first entry)

HIV-1 Vpr protein.

HIV-1 Vpr: human immunodeficiency virus; hyperproliferative disease;  
 cell proliferation.

Human immunodeficiency virus type 1.

W090412-AL:

25-FEB-1999.

14-AUG-1998: 98WO-0516890.

14-AUG-1997: 97US-0055754.

(HYPE) HRIV FERNETVANIA.

Ayazoo V, Kibbet-Elimans T, Mahalingam S, Patel M;  
 Weiner DB.

W01: 1999-181154/15.

Conjugate composition comprising HIV-1 Vpr protein fragment - used

to inhibit cell proliferation, and treating hyperproliferative

diseases

Example: Fig 1A: 64pp: English.

The present invention describes a conjugate composition comprising a fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic compound. The conjugate can be used in a method for inhibiting cell proliferation. It can also be used for treating an individual who has a hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein fragments can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents a HIV-1 Vpr protein sequence.

Sequence: 96 AA:

Query Match: 100.0%; Score: 26; DB: 20; Length: 96;  
 Best Local Similarity: 100.0%; Pred. No. 8, 26-19;

Matches: 26; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 ALKRLDQQLFHFRRGCRSRGII 26  
 59 a1111q1111h1h1h1h1h1h1 84

RESULT: 4

AAW99815: 100.0%; Score: 26; DB: 20; Length: 96;  
 ID: AAW99815 standard: protein; 96 AA.

AAW99815:

08-JUN-1999 (first entry)

HIV Vpr wt protein sequence.

HIV-1 Vpr: human immunodeficiency virus; hyperproliferative disease;  
 cell proliferation.

Human immunodeficiency virus.

W0909412-AL:

25-FEB-1999.

14-AUG-1998: 98WO-0516890.

14-AUG-1997: 97US-0055754.

(HYPE) HRIV FERNETVANIA.

Ayazoo V, Kibbet-Elimans T, Mahalingam S, Patel M;  
 Weiner DB.

W01: 1999-181154/15.

Conjugate composition comprising HIV-1 Vpr protein fragment - used

to inhibit cell proliferation, and treating hyperproliferative

diseases

Example: Fig 1b: 64pp: English.

The present invention describes a conjugate composition comprising a fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic compound. The conjugate can be used in a method for inhibiting cell proliferation. It can also be used for treating an individual who has a hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein fragments can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents an HIV protein sequence.

Sequence: 96 AA:

Query Match: 100.0%; Score: 26; DB: 20; Length: 96;  
 Best Local Similarity: 100.0%; Pred. No. 8, 26-19;  
 Matches: 26; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 ALKRLDQQLFHFRRGCRSRGII 26  
 59 a1111q1111h1h1h1h1h1h1 84

RESULT: 4

AAW99815: 100.0%; Score: 26; DB: 20; Length: 96;  
 ID: AAW99815 standard: protein; 96 AA.

AAW99815:

08-JUN-1999 (first entry)

HIV E21, 24P protein sequence.

```

XX HIV Vpr, Ectod. immunodeficiency virus, hyperproliferative disease,
FM cell proliferation.
KM
XX Human immunodeficiency virus.
GS
FM W69909412-A1.
XX
XX 25-FEB-1999.
PD
XX
XX 14-AUG-1998; 98WO-0516890.
XX
XX 14-AUG-1997; 97US-0055754.
XX
XX (DUP-) UNIV PENNSYLVANIA.
PA
XX
XX Ayyappa V, Kieber Emmons T, Mahalingam S, Patel M,
P1 Weiner DB;
XX
XX WPI: 1999-181154/15.
XX
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
P1 to inhibit cell proliferation, and treating hyperproliferative
PT diseases
XX
XX Example: Fig 1b, 64pp; English
XX
XX The present invention describes a conjugate composition comprising a
CC fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
CC compound. The conjugate can be used in a method for inhibiting cell
CC proliferation. It can also be used for treating an individual who has a
CC hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
CC fragments can be used for identifying compounds that inhibit Vpr protein
CC binding to the p6 domain of p55 or to p6 protein. The present sequence
CC represents an HIV protein sequence.
XX
XX Sequence 96 AA:
SQ

```

Query Match: 100.0%; Score 26; DB 20; Length 96;  
 Post local similarity 100.0%; Pred. No. 8, 2e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIKILQGLIFHRIQSGMSRIGII 26  
 |||||||  
 DB 59 alrikilqglifhriqsgmsrll 84

RESULT 5  
 ID AAW99817 standard; protein; 96 AA.  
 XX  
 XX AAW99817;  
 AC  
 XX 08-JUN-1999 (first entry)  
 PD  
 XX HIV alpha-A protein sequence.  
 DE  
 XX HIV Vpr; human immunodeficiency virus; hyperproliferative disease;  
 FM cell proliferation.  
 KM  
 XX Human immunodeficiency virus.  
 GS  
 FM W69909412-A1.  
 XX  
 XX 25-FEB-1999.  
 PD  
 XX 14-AUG-1998; 98WO-0516890.  
 XX  
 XX 14-AUG-1997; 97US-0055754.  
 XX  
 XX (DUP-) UNIV PENNSYLVANIA.  
 PA  
 XX

```

E1 Ayyappa V, Kieber Emmons T, Mahalingam S, Patel M;
F1 Weiner DB;
XX
XX WPI: 1999-181154/15.
XX
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
CC to inhibit cell proliferation, and treating hyperproliferative
CC diseases
XX
XX Example: Fig 1b, 64pp; English.
XX
XX The present invention describes a conjugate composition comprising a
CC fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
CC compound. The conjugate can be used in a method for inhibiting cell
CC proliferation. It can also be used for treating an individual who has a
CC hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
CC fragments can be used for identifying compounds that inhibit Vpr protein
CC binding to the p6 domain of p55 or to p6 protein. The present sequence
CC represents an HIV protein sequence.
XX
XX Sequence 96 AA:
SQ

```

Query Match: 100.0%; Score 26; DB 20; Length 96;  
 Post local similarity 100.0%; Pred. No. 8, 2e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIKILQGLIFHRIQSGMSRIGII 26  
 |||||||  
 DB 59 alrikilqglifhriqsgmsrll 84

RESULT 6  
 ID AAW99818 standard; protein; 96 AA.  
 XX  
 XX AAW99818;  
 AC  
 XX 08-JUN-1999 (first entry)  
 PD  
 XX HIV A30S protein sequence.  
 DE  
 XX HIV Vpr; human immunodeficiency virus; hyperproliferative disease;  
 FM cell proliferation.  
 KM  
 XX Human immunodeficiency virus.  
 GS  
 FM W69909412-A1.  
 XX  
 XX 25-FEB-1999.  
 PD  
 XX 14-AUG-1998; 98WO-0516890.  
 XX  
 XX 14-AUG-1997; 97US-0055754.  
 XX  
 XX (DUP-) UNIV PENNSYLVANIA.  
 PA  
 XX  
 XX Ayyappa V, Kieber Emmons T, Mahalingam S, Patel M;  
 F1 Weiner DB;  
 XX  
 XX WPI: 1999-181154/15.  
 XX  
 XX Conjugate composition comprising HIV-1 Vpr protein fragment - used  
 CC to inhibit cell proliferation, and treating hyperproliferative  
 CC diseases  
 XX  
 XX Example: Fig 1b, 64pp; English.  
 XX  
 XX The present invention describes a conjugate composition comprising a  
 CC fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic  
 CC compound. The conjugate can be used in a method for inhibiting cell  
 CC proliferation. It can also be used for treating an individual who has a  
 CC hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein  
 CC fragments can be used for identifying compounds that inhibit Vpr protein  
 CC binding to the p6 domain of p55 or to p6 protein. The present sequence  
 CC represents an HIV protein sequence.









Best Local Similarity 100.0%; Prod. No. 7.2e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 PRLIQLLEPHRIGCRHSRIQ 24  
|||||  
61 IRIQLLIIIRIQRHSRIQ 82

RESULT 14

AAM53040  
ID AAM53040 standard; peptide: 96 AA.

AC AAM53040;

DT 17-JUL-1998 (first entry)

DE HIV-1 polypeptide.

KM Recombinant plant virus; HIV-1; protein production; immunisation;  
KM fusion capsid protein; HIV-1; mosaic virus; character; pattern;

KM Thadovirus.

US Human immunodeficiency virus type 1

PN W09808375-A1.

PD 05-MAR-1998.

PF 28-AUG-1997; 92WD-0815200

PP 28-AUG-1997; 92WD-074456

PA (UNDE-) UNIV JEFFERSON THOMAS.

PI Hooper DC, Koprowski H, Madeliska A, Yushov V;

DK WPI, 1998-179070/16.

PT Production of polypeptides, particularly for use in immunisation by  
PT expression as fusions with plant fusion capsid protein in  
PI plant cells infected with virus

PS Miscellaneous; Page 4; 42FF; English.

This sequence is a HIV-1 polypeptide that can be used in a recombinant plant virus used in the process of the invention. The process is for administering a polypeptide to an animal comprising: (a) infecting a plant cell with recombinant plant virus nucleic acid that will be processed in a plant cell to produce a fusion capsid protein (FVP). The FVP comprises a plant virus capsid protein (VCP) and a polypeptide that is not a FVP, the FVP being an affinity reagent virus (ARV) capsid protein (CP) or a derivative thereof creating a infected cell; (b) culturing the infected cell or a derivative cell derived from the infected cell under conditions where the infected cell or derivative cell makes the FVP, and (c) administering the FVP or a portion to an animal. The recombinant plant virus can also be used for production of polypeptides. The method is used particularly for the production of polypeptides which can be used for immunisation against pathogens such as Thadovirus or HIV.

XX Sequence 96 AA;

Query Match 84.6%; Score 22; DB 19; Length 96;

Best Local Similarity 100.0%; Prod. No. 7.2e-15;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 PRLIQLLEPHRIGCRHSRIQ 24  
|||||  
61 IRIQLLIIIRIQRHSRIQ 82

RESULT 15

AAB10685  
ID AAB10685 standard; peptide: 96 AA.

AC AAB10685;

DT 19 JAN-2001 (first entry)

DE HIV-1 regulatory virus protein R peptide svp1-96.

KM Regulatory virus protein R (Vpr) act viral; gene therapy;

KM Pathogenicity; structural analysis; cell cycle arrest.

OS Synthetic.

OS Human immunodeficiency virus type 1.

PN W0200049038-A2.

PD 24-AUG-2000.

PF 19-FEB-2000; 2000W1-090955.

PP 19-FEB-1999; 99DE-1008752.

PA (SCHU/) SCHUBERT U.

PA (HENK/) HENKLEIN P.

PA (WRAV/) WRAV V.

PI Schabert U, Henklein P, Wray V;

DK WPI, 2000-065457/52.

PT New synthetic peptides from the Vpr protein of human immune deficiency virus, useful e.g. for therapy and diagnosis, have good solubility in water.

Claim 3.1: Page 5; 35pp; German.  
This invention describes novel synthetic peptides (I) derived from the regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-1) which have antiviral activity and can be used for gene therapy. (I) is used for therapeutic and/or diagnostic purposes, especially in biological assays, for development of serological tests, enzyme-linked immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in blood), to raise specific antibodies and antisera (especially those reactive with specific epitopes), and as antiviral agents. (I) can also be used in screening for potential Vpr antagonists (i.e. compounds that modulate interaction of Vpr with cellular factors, transcription/translation properties of Vpr, transport of Vpr and its incorporation into viral particles, Vpr induced cell cycle arrest, and cytoxic and/or cytotoxic activities of Vpr). (I) is used to establish cell or animal models for studying pathogenicity of Vpr, for structural analysis of Vpr and its domains, for in vitro assembly of new vectors for gene therapy, as vectors in vitro for complementing the function of Vpr-derived mutants in cell cultures, and to reduce flexibility of Vpr induced by the R limited domain. Synthetic (I) are soluble in water and can be formulated as highly concentrated solutions (molar) without protein aggregation, so are well suited to analysis by nuclear magnetic resonance, X ray or circular dichroism techniques. (I) adopt a folded structure, have biological activity comparable to that of viral Vpr, and can be produced, at high purity, on the milligram scale. This sequence represents the synthetic HIV-1 derived Vpr peptide svp1-96 which is used in the method of the invention.

XX Sequence 96 AA;

Query Match 84.6%; Score 22; DB 21; Length 96;

Best Local Similarity 100.0%; Prod. No. 7.2e-15;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 PRLIQLLEPHRIGCRHSRIQ 24  
|||||

Wed Oct 3 13:40:08 2001

us-09-485-421-1\_copy\_59\_84.rag

Page 8

Job 01 11/04/01 11:04:08 AM

Search completed: not done - 02/20/01 14:25:01  
Job 1 Time: 100.800

GenCore version 4.5  
Copyright (c) 1993 - 2000 GenCore Inc.

1. protein search, using SW model

protein: us-09-485-421-1\_copy\_17\_36 (without alignment)

Search time: 17.68 seconds

Title: us-09-485-421-1\_copy\_17\_36

Sequence: 1 TWLELELEKNAVHPPR 20

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Scanned: 94435 seqs, 4425486 residues

Word size: 0

1. total number of hits satisfying chosen parameters: 94435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database: SwissProt.v3.\*

Prod. No. is the number of results predicted by chosen to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	95.0	78	1	VPR_HV1B1	P05926 human immun
2	19	95.0	78	1	VPR_HV1B5	P05927 human immun
3	19	95.0	96	1	VPR_HV1B8	P05928 human immun
4	19	95.0	96	1	VPR_HV1B9	P20982 human immun
5	17	85.0	96	1	VPR_HV1N8	P05960 human immun
6	14	78.0	96	1	VPR_HV1C2	P22282 chimpanzee
7	10	50.0	96	1	VPR_HV1B9A	P05965 human immun
8	10	50.0	96	1	VPR_HV1N5	P12540 human immun
9	10	50.0	96	1	VPR_HV1C7	P05961 human immun
10	10	50.0	96	1	VPR_HV1M1	P05964 human immun
11	10	50.0	96	1	VPR_HV1Z2	P12545 human immun
12	10	50.0	97	1	VPR_HV1A2	P05962 human immun
13	10	50.0	97	1	VPR_HV1Y2	P12567 human immun
14	8	40.0	96	1	VPR_HV1E1	P05966 human immun
15	8	40.0	96	1	VPR_HV1S1	P05961 human immun
16	8	40.0	65	1	VPR_HV1C1	P46722 escherichia
17	7	35.0	495	1	VPR_HV1C3	P05963 bacillus st
18	7	35.0	495	1	VPR_HV1C4	P12546 bacillus st
19	7	35.0	471	1	VPR_HV1C5	P22283 bacillus st
20	7	35.0	647	1	VPR_HV1C6	P22284 bacillus st
21	5	20.0	51	1	VPR_HV1C7	P22285 bacillus st
22	5	20.0	64	1	VPR_HV1C8	P22286 bacillus st
23	5	20.0	70	1	VPR_HV1C9	P22287 bacillus st
24	5	20.0	125	1	VPR_HV1C10	P22288 bacillus st
25	5	20.0	125	1	VPR_HV1C11	P22289 bacillus st
26	5	20.0	155	1	VPR_HV1C12	P22290 bacillus st
27	5	20.0	155	1	VPR_HV1C13	P22291 bacillus st
28	5	20.0	155	1	VPR_HV1C14	P22292 bacillus st
29	5	20.0	171	1	VPR_HV1C15	P22293 bacillus st
30	5	20.0	174	1	VPR_HV1C16	P22294 bacillus st
31	5	20.0	181	1	VPR_HV1C17	P22295 bacillus st
32	5	20.0	181	1	VPR_HV1C18	P22296 bacillus st
33	5	20.0	181	1	VPR_HV1C19	P22297 bacillus st
34	5	20.0	181	1	VPR_HV1C20	P22298 bacillus st

## ALIGNMENTS

Result ID	Query Match	Length	DB	ID	Description
1	95.0	78	1	VPR_HV1B1	P05926 human immun
2	95.0	78	1	VPR_HV1B5	P05927 human immun
3	95.0	96	1	VPR_HV1B8	P05928 human immun
4	95.0	96	1	VPR_HV1B9	P20982 human immun
5	85.0	96	1	VPR_HV1N8	P05960 human immun
6	78.0	96	1	VPR_HV1C2	P22282 chimpanzee
7	50.0	96	1	VPR_HV1B9A	P05965 human immun
8	50.0	96	1	VPR_HV1N5	P12540 human immun
9	50.0	96	1	VPR_HV1C7	P05961 human immun
10	50.0	96	1	VPR_HV1M1	P05964 human immun
11	50.0	96	1	VPR_HV1Z2	P12545 human immun
12	50.0	97	1	VPR_HV1A2	P05962 human immun
13	50.0	97	1	VPR_HV1Y2	P12567 human immun
14	40.0	96	1	VPR_HV1E1	P05966 human immun
15	40.0	96	1	VPR_HV1S1	P05961 human immun
16	40.0	65	1	VPR_HV1C1	P46722 escherichia
17	35.0	495	1	VPR_HV1C3	P05963 bacillus st
18	35.0	495	1	VPR_HV1C4	P12546 bacillus st
19	35.0	471	1	VPR_HV1C5	P22283 bacillus st
20	35.0	647	1	VPR_HV1C6	P22284 bacillus st
21	20.0	51	1	VPR_HV1C7	P22285 bacillus st
22	20.0	64	1	VPR_HV1C8	P22286 bacillus st
23	20.0	70	1	VPR_HV1C9	P22287 bacillus st
24	20.0	125	1	VPR_HV1C10	P22288 bacillus st
25	20.0	125	1	VPR_HV1C11	P22289 bacillus st
26	20.0	155	1	VPR_HV1C12	P22290 bacillus st
27	20.0	155	1	VPR_HV1C13	P22291 bacillus st
28	20.0	155	1	VPR_HV1C14	P22292 bacillus st
29	20.0	171	1	VPR_HV1C15	P22293 bacillus st
30	20.0	174	1	VPR_HV1C16	P22294 bacillus st
31	20.0	181	1	VPR_HV1C17	P22295 bacillus st
32	20.0	181	1	VPR_HV1C18	P22296 bacillus st
33	20.0	181	1	VPR_HV1C19	P22297 bacillus st
34	20.0	181	1	VPR_HV1C20	P22298 bacillus st



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VPR_HV1JR
ID VPR_HV1JR STANDARD PRT 96 AA
AC P20883
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-JUL-1993 (Rel. 25, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (T-cell isolate) (HIV-1).
OC Virus; Retroviridae; Lentivirinae; Lentiviruses.
OX NCBI_TaxID:11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen L.S.Y.
RL Submitted (DEC-1988) to the HIV data bank.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M38429; AB02747.1;
DR HIV: M38429; VPRSJRCSE.
DR InterPro: IPR000012;
DR Pfam: PF00522; VPR_1
DR PRINTS: PR00444; HIVPRVPX
KW AIDS.
SQ SEQUENCE 96 AA 11419 MW 66545728H2927 CPG64;

Query Match 96.0%, Score 19, FR 1, Length 96;
Best local Similarity 100.0%, Prod No 60-12;
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 WLELELNKNEAVRHP 20
ID 18 WLELELNKNEAVRHP 36

RESULT 5
VPR_HV1JM
ID VPR_HV1JM STANDARD PRT 96 AA
AC P05950;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUL-1993 (Rel. 25, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Virus; Retroviridae; Lentivirinae; Lentiviruses.
OX NCBI_TaxID:11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Mudd J., Gao H.-G., Paredes R., Aldrovini A., Collier A.C.,
RA Parrelli K., Wong-Staal F., Gallo R.C., Weiss M.S. et al.
RT "Envelope sequences of two new United States HIV-1 isolates."
RL Virology 194:531-536(1988).
CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -----
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CC -----
EMBL: M17449; AAA44855.1;

```

```

DR HIV: M17449; VPRSMN.
DE InterPro: IPR000012;
DR Pfam: PF00522; VPR_1.
DR PRINTS: PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA 11344 MW 270514527993E CPG64;

Query Match 85.0%, Score 17, FR 1, Length 96;
Best local Similarity 100.0%, Prod No 490-10;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 LLELELNKNEAVRHP 20
ID 20 LLELELNKNEAVRHP 36

RESULT 6
VPR_SIVCZ
ID VPR_SIVCZ STANDARD PRT 96 AA
AC P12877;
DT 01-NOV-1990 (Rel. 15, Created)
DT 01-NOV-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Chimpanzee immunodeficiency virus (SIV-CPZ) (CIV).
OC Virus; Retroviridae; Lentivirinae; Lentiviruses.
OX NCBI_TaxID:11723;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:9025077; PubMed:2188136;
RA Hueb T., Cheynier P., Meyers R., Roelants G., Main-Hodson S.;
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1."
RT Nature 345:356-359(1990).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X52154; CAAC3403.1;
DR PIR: S09986; ASLJSC.
DR HIV: X52154; VPRSCPE.
RT InterPro: IPR000012;
DR Pfam: PF00522; VPR_1.
DR PRINTS: PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA 11376 MW 16016544CDEFTMS CPG64;

Query Match 70.0%, Score 14, FR 1, Length 96;
Best local Similarity 100.0%, Prod No 360-07;
Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 7 LLELELNKNEAVRHP 20
ID 23 LLELELNKNEAVRHP 36

RESULT 7
VPR_HV1MA
ID VPR_HV1MA STANDARD PRT 96 AA
AC P05955;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUL-1993 (Rel. 25, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).

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[illegible]

Method	Conservative	Mismatches	Indels	Gaps
QY 2 WTELELEEK 11 1111111111	0	0	0	0
LB 13 WTELELEEK 27	0	0	0	0
RESULT 9 VPR HIV09	0	0	0	0
ID VPR HIV09	STANDARD:	PRT:	96 AA.	
AC P20841:				
DI 01 FEB-1991 (Ref. 17, 'Created)				
DI 01 FEB-1991 (Ref. 17, Last sequence update)				
DI 01-JUL-1993 (Ref. 26, Last annotation update)				
DI VPR PROTEIN (R ORF PROTEIN).				
DI VPR.				
OS Human immunodeficiency virus (type 1 (OY1 isolate) (HIV-1).				
OS Viruses: betadelta viruses: Retroviridae: Lentivirinae.				
OX Nhl_1axid.11699;				
OX Nhl_1axid.11699;				
OX Nhl_1axid.11699;				
SEQUENCE FROM N.A.				
KA MELINE 90148544: PubMed2559749;				
KA Hui-1, Duzza M.C., Brim-Verneel F., Boulouis V.E., Malin-Hudson S.L.				
KA "A highly effective HIV-1 strain isolated from a healthy Caucasian				
KA individual presenting an atypical western blot."				
KA AIDS 1997;71:(1989).				
KA 1 MISCELLANEOUS: THE OY1 ISOLATE WAS TAKEN FROM THE BLOOD OF A				
KA HEALTHY CAUCASIAN INDIVIDUAL.				
OS This SWISS-PROT entry is copyright. It is produced through a collaboration				
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OS entities requires a licence agreement. See http://www.ebi.ac.uk/seqdb/				
OS or send an email to license@sb.scrib.ch).				
DI EMBL: M56727; AAN63394.1; .				
DI HIV: M26727; VPR001.				
DI RefSeqID: PR000012; .				
DI Pfam: PF005422; VPR; 1.				
DI PRINTS: PR00444; HIVVPRVX.				
DI AIDS.				
DI STUDENCE 96 AA: 11494 MW: 27080416.95482 CR644;				
OS ONLY MATCH:	59.0%;	Score 10;	DB 1;	Length 96;
OS Best local Similarity 100.0%;	Pf01.	No. 9.0024;		
OS Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 2 WTELELEEK 11 1111111111	0	0	0	0
LB 13 WTELELEEK 27	0	0	0	0
RESULT 10 VPR HIV10	0	0	0	0
ID VPR HIV10	STANDARD:	PRT:	96 AA.	
AC P20944:				
DI 01 MAY-1990 (Ref. 07, 'Created)				
DI 01 MAY-1990 (Ref. 07, Last sequence update)				
DI 01-JUL-1993 (Ref. 26, Last annotation update)				
DI VPR PROTEIN (R ORF PROTEIN).				
DI VPR.				
OS Human immunodeficiency virus (type 1 (H2781 isolate) (HIV-1).				
OS Viruses: betadelta viruses: Retroviridae: Lentivirinae.				
OX Nhl_1axid.11701;				
OX Nhl_1axid.11701;				
OX Nhl_1axid.11701;				
SEQUENCE FROM N.A.				
KA Starich B.F., Rubin B.H., Shaw G.M., McNeely P.D., Motrow S.				
KA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.				
KA Wong Stal P.				
KA Submitted (XXX-1987) to the HIV data bank.				

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M17451; AAA5055.1; -
DR HIV: M17451; VPRSF2.
DR InterPro: IPR00012; -
DR Pfam: PF00522; VPR: 1.
DR PRINTS: PR00444; HIVPRVPX.
DR AIDS: -
SQ SEQUENCE 96 AA; 11299 MW; 67644E959A9344 CRC64;

Query Match 50.0%; Score 10; DB 1; Length 96;
Host Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 2 WTELELEIK 11
|||||
DB 18 WTELELEIK 27

RESULT 11
VPR_HV122 STANDARD; PRT; 96 AA.
AC P12519;
DI 01-OCT-1989 (rel 12, Created)
DI 01-OCT-1989 (rel 12, last sequence update)
DI 01-JUL-1994 (rel 26, last annotation update)
LE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (2270C/234 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxId:11683;
RN 11;
RP Theodore T. Buckler-White A.;
RL Submitted (MV-1988) to the HIV data bank.
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CC -----
DR EMBL: M22479; AAA5368.1; -
DR HIV: M22479; VPRSF2F6.
DR InterPro: IPR00012; -
DR Pfam: PF00522; VPR: 1.
DR PRINTS: PR00444; HIVPRVPX.
DR AIDS: -
SQ SEQUENCE 96 AA; 11299 MW; 65674E959A9344 CRC64;

Query Match 50.0%; Score 10; DB 1; Length 96;
Host Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 2 WTELELEIK 11
|||||
DB 18 WTELELEIK 27

RESULT 11
VPR_HV122 STANDARD; PRT; 97 AA.
AC P35967;
DI 01-JUN-1994 (rel 29, Created)
DI 01-JUN-1994 (rel 29, last sequence update)
DI 01-JUN-1994 (rel 29, last annotation update)
LE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (YO-2 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxId:36377;
RN 11;
RP SEQUENCE FROM N.A.
RP MEDLINE:93021987; PubMed 1404605;
KA Li Y., Hut H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
KA Shaw G.M.;
RI "Complete nucleotide sequence, genome organization, and biological
RI properties of a new immunodeficiency virus (YO-2) from a child
RI for limited detectability and complementation."
PI Virol. 55:6587-6600(1992).
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AC P05952;
DI 01-NOV-1988 (rel 09, Created)
DI 01-NOV-1988 (rel 09, last sequence update)
DI 01-JUL-1993 (rel 26, last annotation update)
LE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (ARV-2) isolate (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxId:11685;
RN 11;
RP SEQUENCE FROM N.A.
RP MEDLINE:8509454; PubMed 259227;
KA Sanchez-Pescador R., Power M.D., Barr P.J., Steiner K.S.,
KA Sanchez-Mon M., Brown-Shimer S.L., Lee W.W., Renard A., Randolph A.,
KA Levy J.A., Dina D., Luciw P.A.;
RI "Nucleotide sequence and expression of an AIDS-associated retrovirus
RI (ARV-2)."
PI Science 227:494-492(1985).
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CC -----
DR EMBL: K02007; AAG6878.1; -
DR HIV: K02007; VPRSF2.
DR InterPro: IPR00012; -
DR Pfam: PF00522; VPR: 1.
DR PRINTS: PR00444; HIVPRVPX.
DR AIDS: -
SQ SEQUENCE 97 AA; 11557 MW; 497049FC2A932440 CRC64;

Query Match 50.0%; Score 10; DB 1; Length 97;
Host Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 2 WTELELEIK 11
|||||
DB 18 WTELELEIK 27

RESULT 11
VPR_HV122 STANDARD; PRT; 97 AA.
AC P35967;
DI 01-JUN-1994 (rel 29, Created)
DI 01-JUN-1994 (rel 29, last sequence update)
DI 01-JUN-1994 (rel 29, last annotation update)
LE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (YO-2 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxId:36377;
RN 11;
RP SEQUENCE FROM N.A.
RP MEDLINE:93021987; PubMed 1404605;
KA Li Y., Hut H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
KA Shaw G.M.;
RI "Complete nucleotide sequence, genome organization, and biological
RI properties of a new immunodeficiency virus (YO-2) from a child
RI for limited detectability and complementation."
PI Virol. 55:6587-6600(1992).
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CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Follet, Jane E. R.  
REGISTRATION NUMBER: 33,342  
PENDING/ISSUED NUMBER: 0345,3106, 03001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-985-54

Query Match 50.0% Score 13; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1, 20-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 10 LEHRRICRRSR 22  
DB 1 LEHRRICRRSR 13

RESULT 5  
US-08-484-985-54  
Sequence 58, Application US/08481985H  
Patent No. 6001146  
GENERAL INFORMATION:  
APPLICANT: Motte, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patonlin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,499  
FILING DATE: 05-DEC-1994  
CLASSIFICATION: 435  
FEE: APPLICATION: \$1676  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
PENDING/ISSUED NUMBER: 0345,3106, 03001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-985-58

Query Match 50.0% Score 13; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1, 20-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 10 LEHRRICRRSR 22  
DB 1 LEHRRICRRSR 13

RESULT 6  
US-08-470-476-58  
Sequence 58, Application US/08370476  
Patent No. 6153408  
GENERAL INFORMATION:  
APPLICANT: Motte, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
APPLICANT: Lane, Yvonne  
APPLICANT: Ojcius, David  
APPLICANT: Castroue, Armande  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patonlin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,476  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117,575  
FILING DATE: 07-SEP-1993  
APPLICATION NUMBER: US 08/072,787  
FILING DATE: 06-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
PENDING/ISSUED NUMBER: 0345,3106, 03001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-470-476-58



SPF ID: 5  
LENGTH: 78  
TYPE: PRT  
ORGANISM: Human; Immunodeficiency virus type 1  
US-09-124-900-5

Query Match 46.2% Score 120 PP 4 Length 78  
Best Local Similarity 100.0% Prod. No. 5.9e 06  
Matches 127 Conservative 0 Mismatches 0 Indels 0 Gaps 0

CY 14 FRICGHSR 14  
DB 1 FRICGHSR 72

RESULT 10  
US-07-941-662-10  
Sequence 30, Application US/07841662  
Patent No. 5414613

GENERAL INFORMATION:  
APPLICANT: Peterson, Per A  
APPLICANT: Jackson, Michael  
APPLICANT: Lenglade-Demoyen, Pierre  
TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: The Scripps Research Institute  
STREET: 10556 No. 5414613th Torrey Pines Road, TPO 8  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037

COMPUTER PEAKABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-07-941 662  
FILING DATE: 19920219  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Logan, April  
REGISTRATION NUMBER: 33,950  
REFERENCE/DOCKET NUMBER: SPFO001P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-07-841-662-30

Query Match 24.5% Score 9 PP 1 Length 78  
Best Local Similarity 100.0% Prod. No. 1.5e+05  
Matches 9 Conservative 0 Mismatches 0 Indels 0 Gaps 0

CY 14 FRICGHSR 22  
DB 1 FRICGHSR 9

RESULT 11  
US-08-209-797-30  
Sequence 30, Application US/08209797  
Patent No. 5529921

GENERAL INFORMATION:  
APPLICANT: Peterson, Per A  
APPLICANT: Jackson, Michael  
APPLICANT: Lenglade-Demoyen, Pierre  
TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: The Scripps Research Institute  
STREET: 10556 No. 5529921th Torrey Pines Road, TPO 8  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037

COMPUTER PEAKABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-08-209-797  
FILING DATE: 10 MAR 1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/841,662  
FILING DATE: 19-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Logan, April  
REGISTRATION NUMBER: 33,950  
REFERENCE/DOCKET NUMBER: SPFO001P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-209-797-30

Query Match 34.6% Score 9 PP 1 Length 78  
Best Local Similarity 100.0% Prod. No. 1.5e+05  
Matches 9 Conservative 0 Mismatches 0 Indels 0 Gaps 0

CY 14 FRICGHSR 22  
DB 1 FRICGHSR 9

RESULT 12  
US-08-669-685-30  
Sequence 30, Application US/08669685  
Patent No. 5827737

GENERAL INFORMATION:  
APPLICANT: Peterson, Per A  
APPLICANT: Jackson, Michael  
APPLICANT: Lenglade-Demoyen, Pierre  
TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: The Scripps Research Institute  
STREET: 10556 No. 5827737th Torrey Pines Road, TPO 8  
CITY: La Jolla

STATE: California  
 COUNTRY: USA  
 ZIPT: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM pc compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent to release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/485-421  
 FILING DATE:  
 CLASSIFICATION: 435  
 PUBLICATION NUMBER: US 6,250,042  
 FILING DATE: 16 MAR 1998  
 APPLICATION NUMBER: US 6,250,042  
 FILING DATE: 16 FEB 1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Larson, April  
 REGISTRATION NUMBER: 34,950  
 REFERENCE/BOOK NUMBER: SP000010  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (412) 580-1186  
 TELEFAX: (412) 580-1189  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MULTIPLE TYPE: peptide  
 HYDROPHOBICITY: N  
 ANI SENSE: NO  
 FRAGMENT TYPE: internal  
 US-09-485-421

Query Match 44.4% Score 92 DB 42 Length 92  
 Post Local Similarity 100.0% Ident. No. 1.5e+05  
 Matches 92 Conservative 02 Mismatches 02 Indels 02 Gaps 02

OY 14 FRICRHSR 22  
 DB 1 FRICRHSR 9

RESULT 14  
 US-09-103-486-40  
 Sequence 41, Application US/09/103-486  
 Patent No. 6,250,042  
 GENERAL INFORMATION:  
 APPLICANT: Peterson, Joel A  
 APPLICANT: Jackson, Michael  
 APPLICANT: Brumark, Anders  
 TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: The Scripps Research Institute  
 STREET: 10550 No. 601 60th Torrey Pines Road, Box 8  
 CITY: La Jolla  
 STATE: California  
 COUNTRY: USA  
 ZIPT: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM pc compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent to release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/103-486  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/485-421  
 FILING DATE: 16-FEB-1998  
 APPLICATION NUMBER: US 6,250,042  
 FILING DATE: 16-FEB-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Larson, April  
 REGISTRATION NUMBER: 34,950  
 REFERENCE/BOOK NUMBER: SP000010  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (412) 580-1186  
 TELEFAX: (412) 580-1189  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MULTIPLE TYPE: peptide  
 HYDROPHOBICITY: N  
 ANI SENSE: NO  
 FRAGMENT TYPE: internal  
 US-09-103-486-40

Query Match 44.4% Score 92 DB 42 Length 92  
 Post Local Similarity 100.0% Ident. No. 1.5e+05  
 Matches 92 Conservative 02 Mismatches 02 Indels 02 Gaps 02

OY 14 FRICRHSR 22  
 DB 1 FRICRHSR 9

RESULT 14  
 US-09-049-982A-41  
 Sequence 41, Application US/09/049-982A  
 Patent No. 6,250,042  
 GENERAL INFORMATION:  
 APPLICANT: Cal, Zoelof  
 APPLICANT: Spren, Jonathan  
 APPLICANT: Brumark, Anders  
 APPLICANT: Jackson, Michael  
 TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-C  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Olson & Hovel, Ltd.  
 STREET: 20 No. 6,250,042th Market Drive, Suite 4000  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIPT: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM pc compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent to release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/049-982A  
 FILING DATE: 16-MAR-1998  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olson, Arno M.  
 REGISTRATION NUMBER: 40,204  
 REFERENCE/BOOK NUMBER: 1SR4710  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (412) 580-1186  
 TELEFAX: (412) 580-1189  
 INFORMATION FOR SEQ ID NO: 41:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 US-09-039-982A-41

Search completed: October 3, 2001, 13:25:46  
 Job Time: 124 sec

Query Match 34.6%; Score 9; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FRIGCRHSR 22  
 |||||  
 DB 1 FRIGCRHSR 9

RESULT 15  
 US-09-039-641-41  
 : Sequence 41, Application US/09039641  
 : Patent No. 6251627  
 : GENERAL INFORMATION:  
 : APPLICANT: Cal, Zelig  
 : APPLICANT: Sprent, Jonathan  
 : APPLICANT: Brumack, Anders  
 : APPLICANT: Jackson, Michael  
 : APPLICANT: Peterson, Per A  
 : TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR  
 : TITLE OF INVENTION: ACTIVATION OF T-CELLS  
 : NUMBER OF SEQUENCES: 45  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Olson & Hierl, Ltd.  
 : STREET: 20 No. 6251627th Wacker Drive, Suite 3000  
 : CITY: Chicago  
 : STATE: Illinois  
 : COUNTRY: USA  
 : ZIP: 60606  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1 0, Version #1 25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/99/039,641  
 : FILING DATE: 8-MAR-1995  
 : CLASSIFICATION:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Olson, Arne M.  
 : REGISTRATION NUMBER: 30,203  
 : REFERENCE/DESCRIPT NUMBER: TSRI4710  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (312) 580-1180  
 : TELEFAX: (312) 580-1189  
 : INFORMATION FOR SEQ ID NO. 41:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 9 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : HYPOTHETICAL: NO  
 : ANTI-SENSE: NO  
 : FRAGMENT TYPE: internal  
 : US-09-039-641-41

Query Match 34.6%; Score 9; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FRIGCRHSR 22  
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 DB 1 FRIGCRHSR 9

Wed Oct 3 13:40:09 2001

us-09-485-421-1\_copy\_59\_84.ra1

Page 8



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OM protein - protein search, using SW model

[illegible]

Title:	US-99-485-421-1_COPY_59_84
Period covered:	76

Sequence: 1 AATPLQJLETHRTCRHSRIGI 26

Çäpür 60.0 , Çäpext 60.0

Searched: 219241 seqs, 76174552 residues

WORD SIZE : 0

Total number of hits satisfying chosen parameters: 21524

Maximum EB seq length: 2000000000

Post-processing: listing first 45 summaries

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Database :
  hph-gg : *
  j-cir  : *
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3.  $\frac{1}{2}$  4.  $\frac{1}{2}$

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	Pos	Description
	1	24	89.5	95	2	vpr protein - huma
	2	18	69.2	96	2	vpr protein - huma
	3	16	61.5	96	1	vpr protein - huma
	4	16	61.5	97	1	vpr protein - huma
	5	14	59.0	96	2	vpr protein - huma
	6	14	59.0	96	1	vpr protein - simi
	7	7	26.9	356	2	NAIIP HC toxin re
	8	7	26.9	356	2	NAIIP HC toxin re
	9	7	26.9	357	2	NAIIP HC toxin re
	10	7	26.9	357	2	NAIIP HC toxin re
	11	7	26.9	461	2	NAIIP HC toxin re
	12	6	22.1	352	2	NAIIP HC toxin re
	13	6	22.1	37	2	NAIIP HC toxin re
	14	6	23.1	89	2	NAIIP HC toxin re
	15	6	23.1	97	2	NAIIP HC toxin re
	16	6	23.1	98	2	NAIIP HC toxin re
	17	6	23.1	101	1	NAIIP HC toxin re
	18	6	23.1	101	2	NAIIP HC toxin re
	19	6	23.1	104	1	NAIIP HC toxin re
	20	6	23.1	105	1	NAIIP HC toxin re
	21	6	23.1	105	2	NAIIP HC toxin re
	22	6	23.1	125	1	NAIIP HC toxin re
	23	6	23.1	189	2	NAIIP HC toxin re
	24	6	23.1	219	2	NAIIP HC toxin re
	25	6	23.1	239	2	NAIIP HC toxin re
	26	6	23.1	247	2	NAIIP HC toxin re
	27	6	23.1	294	2	NAIIP HC toxin re
	28	6	23.1	304	2	NAIIP HC toxin re
	29	6	23.1	305	2	NAIIP HC toxin re

## ALLIEMENTS

30	AS6354	6	23.1	32.5	2	AG3354	protein p23.20 (1
31	TA1454	6	23.1	32.5	2	TA6454	probab. histidinas
32	TA7247	6	23.1	32.7	2	TA7247	probable histidino
33	970544	6	23.1	30.0	2	970544	probable histidino
34	AT75431	6	23.1	40.3	2	AT75431	ATP-dependent Clp
35	AB3615	6	23.1	43.2	2	AB3615	dibutyryl acid
36	C96759	6	23.1	44.1	2	C96759	protein serine car
37	TA5557	6	23.1	57.5	2	TA5557	potassium channel
38	TA1442	6	23.1	58.3	2	TA1442	Na <sup>+</sup> /K <sup>+</sup> dehydrogense
39	S17671	6	23.1	58.3	2	S17671	protein-tyrosineph
40	SA1011	6	23.1	59.9	2	SA1011	hypothetical prot
41	SA032	6	23.1	60.4	2	SA032	probable amino ac
42	TA5624	6	23.1	64.5	2	TA5624	hypothetical prot
43	SA1846	6	23.1	64.9	2	SA1846	5-aminolevulinat
44	EP590	6	23.1	67.1	2	EP590	hypothetical prot
45	TA5505	6	23.1	70.4	2	TA5505	mitochondri endope

**RESULT** 1  
 109383  
 vpr protein human immunodeficiency virus type 1 (isolate ctrl1)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Vaiety: isolate ctrl1  
 C:Date: 11 Jun 1999 seqscore\_perfection 11 Jun 1999 #cont\_change 21-01-2000  
 C:Accession: T09383  
 R:Michael, N. L.; Chong, G.; d'Arcy, L. A.; Ehrenberg, P. K.; Mariani, R.; Busch, M. P.;  
 C: Virel, G. J. 4248-4246, 1995  
 A:Title: Isolation and sequencing of a human immunodeficiency virus type 1 inserted  
 A:Reference number: Z16654; MIMD:95287475  
 A:Accession: T09383  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-95, SMCD  
 A:Cross-reference: EMBL:U04471; NID:9229440; FIDN:AAA9695.1; FID:9829444  
 C:Genetics:  
 A:Gene: vpr  
 C:Subfamily: AIDS vpr protein  
 C:Keywords: AIDS; Immunodeficiency

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Query Match      88.5% Score 231 P: 2 Length 95:
Post Local Similarity: 88.5% Score 231 P: 2 Length 95:
Matches 23. Conservation 0. Indels 0 Gaps
07 3 TRLDQQLIMIRISGRSPGRI 25
      |||||
Db 61 TRLDQQLIMIRISGRSPRI 83

RESULT 2
S54380      human immunodeficiency virus type 1
              protein
1 Species: human immunodeficiency virus type 1, HIV_1
2 Date: 15 Jul 1995 #sequence_revision 91 Sep 1995 #text_change 20 Sep 1995
3 Accession: S54380
4 (Rothgatter, T.) Rockler White, A.J.
submitted to the EMBL Data Library, July 1989
5 Reference Entry: S54377
6 Accession: S54380
7 Status: Preliminary
8 Molecular Type: genomic RNA
9 Positions: 1-96 cDNA
10 Cross-references: EMBL:M22639, NID-9329377, F01R.AAA45468.1, F01.A329388
11 Superfamily: AIDS protein

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Query Match	99.2%	Score 19	19/2	Length 96					
Best Local Similarity	100.0%	Prot. No.	7.60e12						
Matches	19	Conservative	0	Mismatches	0	Indels	0	Gaps	0









DE PARTIAL PROTEINAL VPR GENE (HML MNT ISOLATE) (FRAGMENT).  
 GN Human immunodeficiency virus type 1  
 CC Virusseq: Retroviral viruses: Part: 116761-167612  
 OX NCBI\_TaxID:116761  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN HML MNT  
 RA Nakagawa R., Koyama K., Compagno G., Patterson P., Boussin F.,  
 RT Mares D., Lacharques G., Lomanto D.,  
 RL Submitted (GenBank) to the EMBL database  
 RL EMBL: Z62104; F060072.1  
 RC STRAIN H9.6  
 RL EMBL: F060522; VPR: 1  
 DR PRINTS: F060444; HIVPRVFX.  
 FT NON TER  
 SQ SEQUENCE 96 AA: 11516 MW: 042656544AFVAV CRG64;

Query Match 100.0% Score 26; DB 14; Length 96;  
 Best Local Similarity 100.0% Prod. No. 2.4e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATRTLOQLPFRIGCPHSRIGII 26  
 DB 59 ATRTLOQLPFRIGCPHSRIGII 84

RESULT 4  
 ID 07405 PRELIMINARY: PRT: 96 AA.  
 AC 07405  
 DT 01 AUG 1998 (EMBL: 07, created)  
 DT 01 AUG 1998 (EMBL: 07, last sequence update)  
 DT 01 OCT 2000 (EMBL: 15, last annotation update)  
 DE PARTIAL PROTEINAL VPR GENE (HML MNT ISOLATE) (FRAGMENT).  
 GN VPR  
 OS Human immunodeficiency virus type 1  
 CC Viruses: Retroviral viruses: Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:116761  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN CHL MNT  
 RA Nakagawa R., Koyama K., Compagno G., Patterson P., Boussin F.,  
 RT Mares D., Lacharques G., Lomanto D.,  
 RL Submitted (GenBank) to the EMBL database  
 RL EMBL: Z62104; F060072.1  
 RC STRAIN H9.6  
 RL EMBL: F060522; VPR: 1  
 DR PRINTS: F060444; HIVPRVFX.  
 FT NON TER  
 SQ SEQUENCE 96 AA: 11516 MW: 042656544AFVAV CRG64;

Query Match 100.0% Score 26; DB 14; Length 96;  
 Best Local Similarity 100.0% Prod. No. 2.4e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATRTLOQLPFRIGCPHSRIGII 26  
 DB 59 ATRTLOQLPFRIGCPHSRIGII 84

RESULT 4  
 ID 07405 PRELIMINARY: PRT: 96 AA.  
 AC 07405  
 DT 01 NOV 1996 (EMBL: 01, created)  
 DT 01 NOV 1996 (EMBL: 01, last sequence update)  
 DT 01 MAY 2000 (EMBL: 15, last annotation update)  
 DE VPR PROTEIN.  
 GN VPR  
 OS Human immunodeficiency virus type 1

OC Viruses: Retroviral viruses: Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:116761  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-89.6  
 RC MEDLINE-95156606; PubMed-7854514;  
 RA Kim P.M., Kolson D., Balliet J.W., Srinivasan A., Collman R.G.,  
 RT "Vsi-independent determinants of macrophage tropism in a primary human  
 RT immunodeficiency virus type 1 isolate."  
 RL J. Virol. 69:1755-1761(1995).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-89.6  
 RC MEDLINE-94059708; PubMed-1433527;  
 RA Collman R., Balliet J.W., Gregory S.A., Friedman H., Kolson D.L.,  
 RA Nathanson N., Srinivasan A.,  
 RT "An infectious molecular clone of an unusual macrophage-tropic and  
 RT highly cytopathic strain of human immunodeficiency virus type 1."  
 DR EMBL: 039462; AAA81039.1  
 DR TRANSFAC: T02399  
 DR RefSeq: U020012  
 DR PRAM: F060522; VPR: 1  
 DR PRINTS: F060444; HIVPRVFX.  
 SQ SEQUENCE 96 AA: 11395 MW: 223807354DFE248 CRG64;

Query Match 100.0% Score 26; DB 14; Length 96;  
 Best Local Similarity 100.0% Prod. No. 2.4e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATRTLOQLPFRIGCPHSRIGII 26  
 DB 59 ATRTLOQLPFRIGCPHSRIGII 84

RESULT 5  
 ID 09E248 PRELIMINARY: PRT: 96 AA.  
 AC 09E248  
 DT 01 MAR 2001 (EMBL: 16, created)  
 DT 01 MAR 2001 (EMBL: 16, last sequence update)  
 DT 01 MAR 2001 (EMBL: 16, last annotation update)  
 DE VPR PROTEIN (FRAGMENT).  
 GN VPR  
 OS Human immunodeficiency virus type 1  
 CC Viruses: Retroviral viruses: Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:116761  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MNT4.2  
 RA Ahmad N., Yedavalli V.S.R.K.,  
 RT "Low Conservation of Functional Domains of Human Immunodeficiency  
 RT Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical  
 RT Transmission."  
 RL Submitted (GenBank) to the EMBL database/GenBank databases.  
 RL EMBL: AF275119; AAC32277.1  
 FT NON TER  
 SQ SEQUENCE 96 AA: 11398 MW: 068096875196810 CRG64;

Query Match 100.0% Score 26; DB 14; Length 96;  
 Best Local Similarity 100.0% Prod. No. 2.4e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATRTLOQLPFRIGCPHSRIGII 26  
 DB 59 ATRTLOQLPFRIGCPHSRIGII 84

RESULT 6  
 ID 09E247 PRELIMINARY: PRT: 96 AA.

AC Q9E247: 01-MAR-2001 (TRENBLER, 16, Created)  
 DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)  
 DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)  
 DE VPR PROTEIN (FRAGMENT).  
 GN VPR.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN MT4.1;  
 RA Ahmad N., Veldavalli V.S.R.K.;  
 RT "Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical Transmission.";  
 RT Submitted (04-2000) to the EMBL/Genbank/JFPP databases.  
 RL EMBL: AF275129; AAC32276.1;  
 DE NON-TER 96  
 FT SEQUENCE 96 AA: 11368 MW: 968952975196810 CRC64;  
 SQ

Query Match 100.0%; Score 26; DI 14; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIRLQQLFHFPRIGCRHSRIGI 26  
 DI 59 ALIRLQQLFHFPRIGCRHSRIGI 84

RESULT 7  
 Q9E246: PRELIMINARY: PRT: 96 AA.  
 DI 01-MAR-2001 (TRENBLER, 16, Created)  
 DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)  
 DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)  
 DE VPR PROTEIN (FRAGMENT).  
 GN VPR.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN MT4.1;  
 RA Ahmad N., Veldavalli V.S.R.K.;  
 RT "Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical Transmission.";  
 RT Submitted (04-2000) to the EMBL/Genbank/JFPP databases.  
 RL EMBL: AF275129; AAC32276.1;  
 DE NON-TER 96  
 FT SEQUENCE 96 AA: 11368 MW: 968952975196810 CRC64;  
 SQ

Query Match 100.0%; Score 26; DI 14; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIRLQQLFHFPRIGCRHSRIGI 26  
 DI 59 ALIRLQQLFHFPRIGCRHSRIGI 84

RESULT 8  
 Q9E245: PRELIMINARY: PRT: 96 AA.  
 DI 01-MAR-2001 (TRENBLER, 16, Created)  
 DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)  
 DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)  
 DE VPR PROTEIN (FRAGMENT).  
 GN VPR.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID:11676;  
 RN [1]

GN VPR.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MT4.1;  
 RA Ahmad N., Veldavalli V.S.R.K.;  
 RT "Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical Transmission.";  
 RT Submitted (04-2000) to the EMBL/Genbank/JFPP databases.  
 RL EMBL: AF275129; AAC32280.1;  
 DE NON-TER 96  
 FT SEQUENCE 96 AA: 11368 MW: 968952975196810 CRC64;  
 SQ

Query Match 100.0%; Score 26; DI 14; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIRLQQLFHFPRIGCRHSRIGI 26  
 DI 59 ALIRLQQLFHFPRIGCRHSRIGI 84

RESULT 9  
 Q9E244: PRELIMINARY: PRT: 96 AA.  
 DI 01-MAR-2001 (TRENBLER, 16, Created)  
 DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)  
 DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)  
 DE VPR PROTEIN (FRAGMENT).  
 GN VPR.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MT4.1;  
 RA Ahmad N., Veldavalli V.S.R.K.;  
 RT "Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical Transmission.";  
 RT Submitted (04-2000) to the EMBL/Genbank/JFPP databases.  
 RL EMBL: AF275129; AAC32281.1;  
 DE NON-TER 96  
 FT SEQUENCE 96 AA: 11368 MW: 968952975196810 CRC64;  
 SQ

Query Match 100.0%; Score 26; DI 14; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-19;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIRLQQLFHFPRIGCRHSRIGI 26  
 DI 59 ALIRLQQLFHFPRIGCRHSRIGI 84

RESULT 10  
 Q9E243: PRELIMINARY: PRT: 96 AA.  
 DI 01-MAR-2001 (TRENBLER, 16, Created)  
 DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)  
 DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)  
 DE VPR PROTEIN (FRAGMENT).  
 GN VPR.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID:11676;  
 RN [1]

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RT SEQUENCE FROM N.A.
RT STRAIN MN14.12
BA Ahmad N., Yoshida H., V.S.P.K.
RT Virus type 1 vif and vpr genes correlates with lack of vif/vpr
RT Transmission " "
RT Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases.
RT EMBL: AF275124; ANL32286.1;
RT NON-TER 96
RT SEQUENCE 96 AA: 11488 MW: 6086928751.66410 CRO74;

Query Match
Best Local Similarity 100.0% Score 26; DB 14; Length 96;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTRLDQGLTFHRRIGGRSRIGII 26
ID 59 ALTRLDQGLTFHRRIGGRSRIGII 84
AC 079241 PRELIMINARY: PRJ 96 AA.

RESULT 11
QY241
ID 079241 PRELIMINARY: PRJ 96 AA.
AC 079241 (EMBLrel, 16, created)
DT 01-MAR-2001 (EMBLrel, 16, last sequence update)
DT 01-MAR-2001 (EMBLrel, 16, last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR
OS Human immunodeficiency virus type 1.
OC Virus; Retroviroidea; Retroviridae; Lentivirus.
ON NCI TaxID 11676;
RN STRAIN MN14.12;
RP SEQUENCE FROM N.A.
BA Ahmad N., Yoshida H., V.S.P.K.
RT Virus type 1 vif and vpr genes correlates with lack of vif/vpr
RT Transmission " "
RT Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases.
RT EMBL: AF275124; ANL32286.1;
RT NON-TER 96
RT SEQUENCE 96 AA: 11488 MW: 6086928751.66410 CRO74;

Query Match
Best Local Similarity 100.0% Score 26; DB 14; Length 96;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTRLDQGLTFHRRIGGRSRIGII 26
ID 59 ALTRLDQGLTFHRRIGGRSRIGII 84
AC 079241 PRELIMINARY: PRJ 96 AA.

RESULT 12
QY240
ID 079240 PRELIMINARY: PRJ 96 AA.
AC 079240 (EMBLrel, 16, created)
DT 01-MAR-2001 (EMBLrel, 16, last sequence update)
DT 01-MAR-2001 (EMBLrel, 16, last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR
OS Human immunodeficiency virus type 1.
OC Virus; Retroviroidea; Retroviridae; Lentivirus.
ON NCI TaxID 11676;
RN STRAIN MN14.12;
RP SEQUENCE FROM N.A.
BA Ahmad N., Yoshida H., V.S.P.K.
RT Virus type 1 vif and vpr genes correlates with lack of vif/vpr
RT Transmission " "
RT Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases.
RT EMBL: AF275124; ANL32286.1;
RT NON-TER 96
RT SEQUENCE 96 AA: 11488 MW: 6086928751.66410 CRO74;

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RT TRANSMISSION " "
RT Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases.
RT EMBL: AF275124; ANL32286.1;
RT NON-TER 96
RT SEQUENCE 96 AA: 11488 MW: 6086928751.66410 CRO74;

Query Match
Best Local Similarity 100.0% Score 26; DB 14; Length 96;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTRLDQGLTFHRRIGGRSRIGII 26
ID 59 ALTRLDQGLTFHRRIGGRSRIGII 84
AC 079249 PRELIMINARY: PRJ 96 AA.

RESULT 13
QY249
ID 079249 PRELIMINARY: PRJ 96 AA.
AC 079249 (EMBLrel, 16, created)
DT 01-MAR-2001 (EMBLrel, 16, last sequence update)
DT 01-MAR-2001 (EMBLrel, 16, last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR
OS Human immunodeficiency virus type 1.
OC Virus; Retroviroidea; Retroviridae; Lentivirus.
ON NCI TaxID 11676;
RN STRAIN MN14.12;
RP SEQUENCE FROM N.A.
BA Ahmad N., Yoshida H., V.S.P.K.
RT Virus type 1 vif and vpr genes correlates with lack of vif/vpr
RT Transmission " "
RT Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases.
RT EMBL: AF275129; ANL32286.1;
RT NON-TER 96
RT SEQUENCE 96 AA: 11488 MW: 6086928751.96410 CRO74;

Query Match
Best Local Similarity 100.0% Score 26; DB 14; Length 96;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTRLDQGLTFHRRIGGRSRIGII 26
ID 59 ALTRLDQGLTFHRRIGGRSRIGII 84
AC 079253 PRELIMINARY: PRJ 96 AA.

RESULT 14
QY253
ID 079253 PRELIMINARY: PRJ 96 AA.
AC 079253 (EMBLrel, 01, created)
DT 01-NOV-1996 (EMBLrel, 01, last sequence update)
DT 01-NOV-1996 (EMBLrel, 01, last annotation update)
DE VPR PROTEIN.
GN VPR
OS Human immunodeficiency virus type 1.
OC Virus; Retroviroidea; Retroviridae; Lentivirus.
ON NCI TaxID 11676;
RN STRAIN PATIENT 4497, HOMOSEXUAL, GERMANY;
BA KATKEE L., GORALISSON E., GORALISSON P., HARTMAN C., CHIBBS J.,
RT Goudsmith J.;
RT J. Gen. Virol. 0:0-0(1996);
RT EMBL: Z68557; CAA92861.1;
RT IndetPro: IP800012;
RT P1am, PF06722, VPR; 1;
RT PRIN1: PR00444; HIVVPRVX;
RT SEQUENCE 94 AA: 11458 MW: 6285918201.28720 CRO74;

```



Query Match 96.2% Score 25; DB 14; length 94;

Best Local Similarity 100.0%; Prod. No. 2,40-18;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 ALRIHLOQLFHFRIQGRHSKIGI 25

UU 59 ALRIHLOQLFHFRIQGRHSKIGI 83

RESULT 15

071918

U 071918 PRELIMINARY: PRT: 95 AA.

AC 071918;

U 01-NOV-1996 (TREMURel. 01, Created)

U 01-NOV-1996 (TREMURel. 01, Last sequence update)

U 01-MAY-2000 (TREMURel. 13, Last annotation update)

U CENTEL 1, CLONE 4, ACCESSORY REGION GENES, COMPLETE CDS.

UN VPR.

US Human immunodeficiency virus type 1

UU Virus(es); Retroviral virus(es); Retroviridae; Lentivirus.

UX NCBI TaxID: 11676;

KN 11

BP SEQUENCE OF 1-20 FROM N.A.

BC STRAIN CENTEL 1; TISSUE-BLOOD;

KX MEDLINE:95287475; PubMed 7769682;

KA Michael N.L., Chang G., d'Arcy L.A., Ehrenberg P.K., Mariani R.,

KA Busch M.P., Marx D.L., Schwartz D.H.;

K1 "Perfectly accessory" gene is a human immunodeficiency virus type 1-

K1 infected lymphoid cell lacking proviral virus."

K1 J. Virol. 69:4228-4236(1995).

KN 121

BP SEQUENCE FROM N.A.

BC STRAIN CENTEL 1; TISSUE-BLOOD;

KA Michael N.L.;

K1 Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

UK EMBL: U24450; A079568.1;

UK InterPro: IPR00012;

UK Pfam: PF00522; VPR: 1;

UK PRINTS: PR00444; HIVVRVFX.

SJ SEQUENCE: 95 AA; 11251 MW; A690D336304C025 CRC64;

Query Match 96.2% Score 25; DB 14; length 95;

Best Local Similarity 100.0%; Prod. No. 2,50-18;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 ALRIHLOQLFHFRIQGRHSKIGI 25

UU 59 ALRIHLOQLFHFRIQGRHSKIGI 83

Search completed: October 3, 2001, 13:30:12  
Job time: 290 sec



GenCorp version 4.5  
Copyright (c) 1993-2000 GenCorp Inc.

OR protein protein search, using sw method

Run on: October 3, 2001, 13:40:32, Search time: 13.68 seconds  
(without alignments)  
65,105,411,000 cells updated/sec

Title: US 09-485-421-1\_COPY\_59\_84

Perfect score: 26

Sequence: 1 ALIRILQDLFTFRIGCRHSRIIG 26

# ALIGNMENTS

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size: 6

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: SWISSPROT\_39\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	92.3	96	1	VPR_HV1MN
2	24	92.3	96	1	VPR_HV1SC
3	23	94.6	96	1	VPR_HV1JP
4	22	94.6	96	1	VPR_HV1PR
5	22	94.6	96	1	VPR_HV1RS
6	18	61.5	96	1	VPR_HV1C2
7	16	61.5	96	1	VPR_HV1EL
8	16	61.5	96	1	VPR_HV1OY
9	16	61.5	96	1	VPR_HV1RH
10	16	61.5	96	1	VPR_HV1A2
11	16	61.5	96	1	VPR_HV1Y2
12	13	50.0	96	1	VPR_HV1MA
13	12	45.2	96	1	VPR_HV1BI
14	12	45.2	96	1	VPR_HV1B5
15	8	30.8	101	1	VPR_SIVC2
16	7	26.9	96	1	VPR_SIVC2
17	7	26.9	96	1	VPR_SIVC2
18	6	23.1	96	1	VPR_SIVC2
19	6	23.1	96	1	VPR_SIVC2
20	6	23.1	101	1	VPR_SIVC2
21	6	23.1	101	1	VPR_SIVC2
22	6	23.1	101	1	VPR_SIVC2
23	6	23.1	101	1	VPR_SIVC2
24	6	23.1	101	1	VPR_SIVC2
25	6	23.1	101	1	VPR_SIVC2
26	6	23.1	101	1	VPR_SIVC2
27	6	23.1	101	1	VPR_SIVC2
28	6	23.1	101	1	VPR_SIVC2
29	6	23.1	101	1	VPR_SIVC2
30	6	23.1	101	1	VPR_SIVC2
31	6	23.1	101	1	VPR_SIVC2
32	6	23.1	101	1	VPR_SIVC2
33	6	23.1	101	1	VPR_SIVC2

34	6	23.1	589	1	Y041_CAEEL
35	6	23.1	694	1	Y041_CAEEL
36	6	23.1	704	1	Y041_CAEEL
37	6	23.1	704	1	Y041_CAEEL
38	6	23.1	704	1	Y041_CAEEL
39	6	23.1	704	1	Y041_CAEEL
40	6	23.1	704	1	Y041_CAEEL
41	6	23.1	704	1	Y041_CAEEL
42	6	23.1	704	1	Y041_CAEEL
43	6	23.1	704	1	Y041_CAEEL
44	6	23.1	704	1	Y041_CAEEL
45	6	23.1	704	1	Y041_CAEEL

RESULT 1  
VPR\_HV1MN STANDARD: PRT: 96 AA.

AC P05950:

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 01-JUL-1993 (Rel. 26, Last annotation update)

DE VPR PROTEIN (R ORF PROTEIN).

GN VPR.

OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).

OW Virusess; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11696;

RN 11

RP SEQUENCE FROM N.A.

FA MPRIN-88210512; PubMed-2369091;

FA Gougo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,

FA Farrel R., Wang S.-L., Salas R., Kelly M.S., Jr.,

FA "Envelope sequences of two new United States HIV-1 isolates."

RI Virology 164:531-536(1988).

CC 1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PATIENT IN 1984.

CC

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DR EMBL: M7449; AAA44855.1; -

DR HIV: M7449; VPRMN.

DE InterPro: IP000012; -

DE Pfam: PF09523; VPR\_1.

DE PRINTS: PP00444; HIVPRVPR.

KW AIDS.

EQ PROQUENCE 96 AA, 11344 MW, 2390377579556P 280642

Query Match: 92.3%, Score: 24, 25 L, Length: 96.

Best Local Similarity: 100.0%, Pred. NO. Ident: 0; Indels: 0; Gaps: 0;

Matches: 24; Conservative: 0; Mismatches: 0;

QY 3 TRILQDLFTFRIGCRHSRIIG 26

TR 61 TRILQDLFTFRIGCRHSRIIG 84

RESULT 2

VPR\_HV1SC STANDARD: PRT: 96 AA.

AC P05951:

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 01-JUL-1993 (Rel. 26, Last annotation update)

DE VPR PROTEIN (R ORF PROTEIN).

GN VPR.

OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).

OW Virusess; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11696;

RN 11

RP SEQUENCE FROM N.A.

FA MPRIN-88210512; PubMed-2369091;

FA Gougo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,

FA Farrel R., Wang S.-L., Salas R., Kelly M.S., Jr.,

FA "Envelope sequences of two new United States HIV-1 isolates."

RI Virology 164:531-536(1988).

CC 1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PATIENT IN 1984.

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CC



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01 05 Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
02 06 Viruses: Retroviral viruses, Retroviridae: Lentivirus.
03 07 NBL_taxid=11698;
04 08 FN
05 09 SEQUENCE FROM N.A.
06 10 Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.J.
07 11 Submitted (FBI 1988) to the EMBL/Genbank/DDBJ databases
08 12
09 13 This SWISS-Prot entry is copyright. It is produced through a collaboration
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14 18 entities requires a license agreement (See http://www.ebi.ac.uk/seqdb/doc/seqdb.html
15 19 or send an email to license@ebi.ac.uk).
16 20
17 21 EMBL: M19921; AAA4590.1;
18 22 HIV: M19921; VERSM14.
19 23 InfoProc: IP000012;
20 24 Plasm: PR00522; VPR: 1.
21 25 PRINTS: PR00444; HIVPRPYX
22 26 AIDS.
23 27 SOURCE: 96 AA; 11380 MW; 55535.65347gDa (CD064).
24 28
25 29 Query Match: 84.6%; Score 22; E: 1; Length 96;
26 30 Best Local Similarity: 100.0%; Prod. No. 1 to 16;
27 31 Match: 16; Conserved: 0; Mismatches: 2; Indels: 0; Gaps: 0.
28 32
29 33 1 ATATTGCTTTCCTGCTGCTT 24
30 34 |||TTTTTTTTTTTTTTTT|||
31 35 Db 61 LRIHQOLEFHPRICRHSKIG 82
32 36
33 37 RESULT 6
34 38 VPR_HIV122
35 39 ID VPR_HIV122 STAN:VPR: PRT: 96 AA.
36 40 P12519;
37 41 D1 01-OCT-1989 (Rel. 12, Created)
38 42 D1 01-OCT-1989 (Rel. 12, Last sequence update)
39 43 D1 01-JUL-1993 (Rel. 26, Last annotation update)
40 44 DE VPR PROTEIN (R ORF PROTEIN).
41 45 GN VPR.
42 46 OS Human immunodeficiency virus type 1 (227/702/224 isolate) (HIV-1).
43 47 VS Viruses: Retroviral viruses, Retroviridae: Lentivirus.
44 48 OX NBL_taxid=11698;
45 49 FN
46 50 SEQUENCE FROM N.A.
47 51 Buckler C.E., Buckler-White A.J.
48 52 Submitted (NOV-1988) to the HIV data bank.
49 53
50 54 This SWISS-Prot entry is copyright. It is produced through a collaboration
51 55 between the Swiss Institute of Bioinformatics and the EMBL outstation at
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53 57 use by non-profit institutions as long as its content is in no way
54 58 modified and this statement is not removed, changed, usage by and for commercial
55 59 entities requires a license agreement (See http://www.ebi.ac.uk/seqdb/doc/seqdb.html
56 60 or send an email to license@ebi.ac.uk).
57 61
58 62 EMBL: M22649; AAA45368.1;
59 63 HIV: M22649; VPR0226.
60 64 InfoProc: IP000012;
61 65 Plasm: PR00522; VPR: 1.
62 66 PRINTS: PR00444; HIVPRPYX.
63 67 AIDS.
64 68 SOURCE: 96 AA; 11380 MW; 55535.65347gDa (CD064).
65 69
66 70 Query Match: 69.2%; Score 18; E: 1; Length 96;
67 71 Best Local Similarity: 100.0%; Prod. No. 26-1;
68 72 Match: 16; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0.
69 73
70 74 1 ATATTGCTTTCCTGCTGCTT 18
71 75

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